

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds

(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HSLRGLFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	82.2	154	12 Q67887	Q67887 hepatitis b
2	37	82.2	453	10 Q9LU91	Q9LU91 arabisopsis
3	37	82.2	453	10 Q8L720	Q8L720 arabisopsis
4	37	82.2	484	16 Q8XLS1	Q8XLS1 clostridium
5	26	80.0	1592	16 Q8XV66	Q8XV66 raistonia s
6	36	80.0	1615	16 Q9RXX2	Q9RXX2 deinococcus
7	35	77.8	66	12 Q67873	Q67873 hepatitis b
8	35	77.8	70	12 Q9YV9	Q9YV9 hepatitis b
9	35	77.8	70	12 Q9W8F3	Q9W8F3 hepatitis b
10	35	77.8	70	12 Q9YJA9	Q9YJA9 hepatitis b
11	35	77.8	70	12 Q9YVW2	Q9YVW2 hepatitis b
12	35	77.8	70	12 Q9WKC7	Q9WKC7 hepatitis b
13	35	77.8	70	12 Q9WKC6	Q9WKC6 hepatitis b
14	35	77.8	95	10 Q9PER0	Q9PER0 zea mays (m
15	35	77.8	97	12 Q9WP57	Q9WP57 hepatitis b
16	35	77.8	100	12 Q9WP61	Q9WP61 hepatitis b

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17 35 77.8 103 12 Q9WP79 hepatitis b
18 35 77.8 103 12 Q9JH71 hepatitis b
19 35 77.8 103 12 Q9WP49 hepatitis b
20 35 77.8 129 12 Q8QVU1 hepatitis b
21 35 77.8 129 12 Q8QVU0 hepatitis b
22 35 77.8 129 12 Q8QVT5 hepatitis b
23 35 77.8 129 12 Q8QVS7 hepatitis b
24 35 77.8 129 12 Q8QVS0 hepatitis b
25 35 77.8 129 12 Q8QVT1 hepatitis b
26 35 77.8 129 12 Q8QVU8 hepatitis b
27 35 77.8 129 12 Q8QVU7 hepatitis b
28 35 77.8 129 12 Q8QVU2 hepatitis b
29 35 77.8 129 12 Q8QVU5 hepatitis b
30 35 77.8 129 12 Q8QVT3 hepatitis b
31 35 77.8 129 12 Q8QVT0 hepatitis b
32 35 77.8 129 12 Q8QVU3 hepatitis b
33 35 77.8 129 12 Q8QVS4 hepatitis b
34 35 77.8 129 12 Q8QVT4 hepatitis b
35 35 77.8 129 12 Q8QVR9 hepatitis b
36 35 77.8 129 12 Q8QVS9 hepatitis b
37 35 77.8 129 12 Q8QVT7 hepatitis b
38 35 77.8 129 12 Q8QVT2 hepatitis b
39 35 77.8 129 12 Q8QVS3 hepatitis b
40 35 77.8 129 12 Q8QVS8 hepatitis b
41 35 77.8 129 12 Q8QVU4 hepatitis b
42 35 77.8 129 12 Q8QVS6 hepatitis b
43 35 77.8 129 12 Q8QVU6 hepatitis b
44 35 77.8 129 12 Q8QVT6 hepatitis b
45 35 77.8 129 12 Q8QVT9 hepatitis b

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ALIGNMENTS

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RESULT 1
Q67887 PRELIMINARY; PRT; 154 AA.
ID Q67887
AC Q67887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein.
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Melis A., Balestrieri A.;
RT "Sequence analysis of HBV genomes isolated from patients with HBsAg
RL negative chronic liver disease.";
RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X68292; CAA48352.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16614 MW; 15F02AB57C8D7681 CRC64;

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Query Match 82.2%; Score 37; DB 12; Length 154;
Best Local Similarity 88.9%; Pred. No. 6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 HSLRGLFV 9
Db 52 HSLRGLTV 60

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RESULT 2
Q9LU91 PRELIMINARY; PRT; 453 AA.
ID Q9LU91
AC Q9LU91;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

```

DE GB|RAD12709.1 (AT3926000/MP111_15).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20277490; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesena E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB023041; BAB01063.1; -;
 DR EMBL; AY058077; RAL24185.1; -;
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 SQ SEQUENCE 453 AA; 50543 MW; CCD32A1DBA9039C4 CRC64;

Query Match 82.2%; Score 37; DB 10; Length 453;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLF 8
 Db 325 HLQRLGLF 332

RESULT 3
 Q8L720 PRELIMINARY; PRT; 453 AA.
 ID Q8L720
 AC Q8L720
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Expressed protein.
 GN AT3G26000
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY140009; RAN98151.1; -;
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.

SO SEQUENCE 453 AA; 50544 MW; CCD32A171A903364 CRC64;
 Query Match 82.2%; Score 37; DB 10; Length 453;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLF 8
 Db 325 HLQRLGLF 332

RESULT 4
 Q8XLS1 PRELIMINARY; PRT; 484 AA.
 ID Q8XLS1
 AC Q8XLS1
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Probable Na⁺/H⁺ antiporter.
 GN CPE0970.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AP003188; BAB80676.1; -;
 DR InterPro; IPR006153; Na⁺ H porter.
 DR InterPro; IPR006037; TrkAC.
 DR Pfam; PF00999; Na⁺ H Exchanger; 1.
 DR Pfam; PF02080; TrkA-C; 1.
 KW Complete proteome.
 SQ SEQUENCE 484 AA; 53525 MW; 5C061DD5A26C0739 CRC64;

Query Match 82.2%; Score 37; DB 16; Length 484;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
 Db 224 HLSVRGAFV 232

RESULT 5
 Q8XV66 PRELIMINARY; PRT; 1582 AA.
 ID Q8XV66
 AC Q8XV66
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Probable glutamate synthase (Large subunit) oxidoreductase protein
 DE (BC 1.4.1.13).
 GN GLTB OR RSC2965 OR RSO1332.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangerot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002);
 DR EMBL; AL646072; CAD16672.1; -;
 DR InterPro; IPR002489; DUF14.
 DR InterPro; IPR002932; Glu_synthase.
 DR InterPro; IPR006981; Glu_synth_NTN.
 DR InterPro; IPR006982; Glu_synth_Central.
 DR Pfam; PF01645; Glu_synthase; 1.
 DR Pfam; PF04897; Glu_synth_NTN; 1.
 DR Pfam; PF04898; Glu_synth_Central; 1.
 DR Pfam; PF01493; GXGXG; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 1582 AA; 173669 MW; 7F5C498FFB59F0E9 CRC64;

Query Match 80.0%; Score 36; DB 16; Length 1582;
 Best Local Similarity 75.0%; Pred.No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGLF 8
 |:::|
 Db 871 HMTLRGLF 878

RESULT 6
 O9RXX2 PRELIMINARY; PRT; 1615 AA.
 AC Q9RXX2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glutamate synthase, large subunit.
 GN DR0183.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RA;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1."
 RT Science 286:1571-1577(1999).
 RL EMBL; AE001880; AAF09770.1; -;
 DR TIGR; DR0183.
 DR InterPro; IPR002489; DUF14.
 DR InterPro; IPR002932; Glu_synthase.
 DR InterPro; IPR006981; Glu_synth_NTN.
 DR InterPro; IPR006982; Glu_synth_Central.
 DR Pfam; PF01645; Glu_synthase; 1.
 DR Pfam; PF04897; Glu_synth_NTN; 1.
 DR Pfam; PF04898; Glu_synth_Central; 1.
 DR Pfam; PF01493; GXGXG; 1.
 KW Complete proteome.
 SQ SEQUENCE 1615 AA; 176918 MW; FE014DB1140BFE26 CRC64;

Query Match 80.0%; Score 36; DB 16; Length 1615;
 Best Local Similarity 75.0%; Pred.No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGLF 8
 |:::|
 Db 890 HMTLRGLF 897

RESULT 7
 Q67873 PRELIMINARY; PRT; 66 AA.
 AC Q67873
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE X ORF.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lai M.E., Mazzoleni A.P., Balestrieri A., Melis A., Porru A.;
 RT "Sequence analysis of HBV genomes isolated from patients with HBsAg
 RT Negative chronic liver disease."
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X65257; CAA46351.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 66 AA; 6701 MW; 2D3923207BFF8E3C CRC64;

Query Match 77.8%; Score 35; DB 12; Length 66;
 Best Local Similarity 100.0%; Pred.No. 6.7; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRGL 7
 |:::|
 Db 52 HLSLRGL 58

RESULT 8
 Q9YFV9 PRELIMINARY; PRT; 70 AA.
 AC Q9YFV9
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261764; PubMed=10799618;
 RA Greche S., Heckel J.O., Rietschel W., Hufert F.T.;
 RT "Molecular epidemiology of hepatitis B virus variants in non-human
 RT primates."
 RL J. Virol. 74:5377-5381(2000).
 DR EMBL; AJ131555; CAA10413.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON_TER 70
 SQ SEQUENCE 70 AA; 7101 MW; B788B4A9B9A5CFF3 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred.No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7
 |:::|
 Db 52 HLSLRGL 58

RESULT 9
 Q9W8F3 PRELIMINARY; PRT; 70 AA.
 AC Q9W8F3
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.

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OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Thomssen R., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131556; CAA10415.1; -.
DR EMBL; AJ131553; CAA10409.1; -.
DR EMBL; AJ131554; CAA10411.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7095 MW; B79CF0F9A3EF7B17 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 10
ID Q9YJA9 PRELIMINARY; PRT; 70 AA.
AC Q9YJA9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Thomssen R., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131558; CAA10419.1; -.
DR EMBL; AJ131557; CAA10417.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7099 MW; B79CF0F9A3EF7F13 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 11
ID Q9YPW2 PRELIMINARY; PRT; 70 AA.
AC Q9YPW2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Hufert F.T.;

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RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL J. Virol. 74:5377-5381(2000).
DR EMBL; AJ131551; CAA10405.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7064 MW; 621D545CA24BD293 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 12
ID Q9WKC7 PRELIMINARY; PRT; 70 AA.
AC Q9WKC7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL J. Virol. 74:5377-5381(2000).
DR EMBL; AJ131548; CAA10399.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70
SQ SEQUENCE 70 AA; 7100 MW; A5114820ECFBD17 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 13
ID Q9WKC6 PRELIMINARY; PRT; 70 AA.
AC Q9WKC6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Grethe S., Heckel J.O., Rietschel W., Hufert F.T.;
RT "Molecular epidemiology of hepatitis B virus variants in non-human
RT primates.";
RL J. Virol. 74:5377-5381(2000).
DR EMBL; AJ131550; CAA10403.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 70

```


SQ SEQUENCE 70 AA; 7128 MW; B99B88D20C89CC0C CRC64;

Query Match 77.8%; Score 35; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 14

Q9PERO PRELIMINARY; PRT; 95 AA.
AC Q9PERO;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Basal layer antifungal peptide precursor.
GN BAP-3B.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Endosperm;
RA Serna Sanz A., Thompson R.D.;
RT "Maize endosperm secretes a novel antifungal protein into adjacent maternal tissue."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ297903; CAC21607.1; -
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 95 BAP-3B PROTEIN.
SQ SEQUENCE 95 AA; 11076 MW; 82B4F67B9512D243 CRC64;

Query Match 77.8%; Score 35; DB 10; Length 95;
Best Local Similarity 55.6%; Pred. No. 9.7; Gaps 0;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
DB 7 HITIRGLFL 15

RESULT 15

Q9WPS7 PRELIMINARY; PRT; 97 AA.
AC Q9WPS7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE X protein.
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1] _
RP SEQUENCE FROM N.A.
RX MEDLINE=20037832; PubMed=10573161;
RA Preikschat P., Meisel H., Will H., Gunther S.;
RT "Hepatitis B virus genomes from long-term immunosuppressed virus carriers are modified by specific mutations in several regions."
RL J. Gen. Virol. 80:2685-2691(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Preikschat P., Meisel H., Iwanska A., Will H., Gunther S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF143306; AAD37956.1; -
DR InterPro; IPR000236; TransactX.
PFam; PF00739; X; 1.

SQ SEQUENCE 97 AA; 10051 MW; 47445E0D2909A897 CRC64;

Query Match 77.8%; Score 35; DB 12; Length 97;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

Search completed: December 23, 2003, 08:46:07
Job time : 27.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HLSLRGLFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 76:*

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	82.2	154	2 S25650	gene X protein - h
2	37	82.2	1436	2 A46496	antigen WC1.1 prec
3	36	80.0	1615	2 C75551	glutamate synthase
4	35	77.8	66	2 S20747	gene X protein - h
5	35	77.8	134	1 B48345	gene X protein, tr
6	35	77.8	154	1 QQVLD1	gene X protein - h
7	35	77.8	154	1 A48345	gene X protein - h
8	35	77.8	154	1 QQVLBH	gene X protein - h
9	35	77.8	154	1 QQVLAI	gene X protein - h
10	35	77.8	154	1 QQVLAW	gene X protein - h
11	35	77.8	154	1 QQVLKS	gene X protein - h
12	35	77.8	154	1 QQVLCF	gene X protein - h
13	35	77.8	154	2 S20756	gene X protein - h
14	35	77.8	154	2 S47404	gene X protein - h
15	35	77.8	154	2 S47408	gene X protein - h
16	35	77.8	154	2 JS0256	gene X protein - h
17	35	77.8	154	2 S67503	gene X protein - h
18	35	77.8	154	2 JQ2228	trans-activating p
19	35	77.8	154	2 S53130	gene X protein - h
20	35	77.8	154	2 JS0603	gene X protein - h
21	35	77.8	154	2 JS0604	gene X protein - h
22	35	77.8	154	2 S35529	gene X protein - h
23	35	77.8	154	2 S33687	gene X protein - h
24	35	77.8	154	2 S12542	gene X protein - h
25	35	77.8	154	2 S32203	gene X protein - h
26	35	77.8	154	2 S23219	gene X protein - h
27	35	77.8	154	2 S20751	gene X protein - h
28	35	77.8	154	2 T13466	gene X protein - h
29	35	77.8	172	2 A58456	X protein - human

30 35 77.8 210 2 T13472 gene X protein - h
31 35 77.8 210 2 S12598 gene X protein - h
32 35 77.8 359 2 S04570 gene X/C fusion pr
33 35 77.8 451 2 G83916 glycolate oxidase
34 34 75.6 178 2 S29119 hypothetical prote
35 34 75.6 361 2 S30325 hypothetical prote
36 34 75.6 1200 2 C96025 hypothetical expor
37 33 73.3 195 2 JC2258 substrate protein
38 33 73.3 569 2 AB0005 probable exported
39 32 71.1 296 2 B83417 hypothetical prote
40 32 71.1 348 2 C81284 cystathionine beta
41 32 71.1 369 2 B75511 dihydroorotate deh
42 32 71.1 430 2 H91259 hypothetical prote
43 32 71.1 430 2 D86100 hypothetical prote
44 32 71.1 430 2 A65215 hypothetical 49.4
45 32 71.1 509 2 B86667 alkyl hydroperoxid

ALIGNMENTS

RESULT 1

S25650 gene X protein - hepatitis B virus (subtype ayw, patient D)

C/Species: hepatitis B virus, HBV

A/Variety: subtype ayw, patient D

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C/Accession: S25650

R/Lai, M.E.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.

submitted to the EMBL Data Library, September 1992

A/Description: Sequence analysis of HSV genomes isolated from patients with HBsAg negati

A/Reference number: S25650

A/Accession: S25650

A/Molecule type: DNA

A/Residues: 1-154 <LAI>

A/Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449

A/Experimental source: subtype ayw, patient D

C/Genetics:

A/Gene: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 82.2%; Score 37; DB 2; Length 154;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
Db 52 HLSLRGLTV 60

RESULT 2

A46496

antigen WC1.1 precursor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 18-Jun-1993 #sequence_revision 19-May-1994 #text_change 05-Nov-1999

C/Accession: A46496; I45834; S19913

R/Wijngaard, P.L.; Metzelaar, M.J.; MacHugh, N.D.; Morrison, W.I.; Clevers, H.C.

J. Immunol. 149, 3273-3277, 1992

A/Title: Molecular characterization of the WC1 antigen expressed specifically on bovine

A/Reference number: A46496; MUID:93056489; PMID:1431105

A/Accession: A46496

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1436 <WJ>

A/Cross-references: EMBL:X63723; NID:g13; PIDN:CAA45255.1; PID:g14

A/Experimental source: CD4-CD8- gamma delta T lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIP:117475)

R/Wijngaard, P.L.; MacHugh, N.D.; Metzelaar, M.J.; Romberg, S.; Bensaid, A.; Pepin, L.;

J. Immunol. 152, 3476-3482, 1994

A/Title: Members of the novel WC1 gene family are differentially expressed on subsets of

A/Reference number: I45834; MUID:94194107; PMID:7511649

A/Accession: I45834

A/Status: preliminary; translated from GS/EMBL/DBU

A:Molecule type: mRNA
A:Residues: 1-1436 <W12>
A:Cross-references: EMBL:X63723; NID:g13; PIDN:CAA45255.1; PID:g14
C:Genetics:
A:Gene: WC1.1
C:Superfamily: scavenger receptor cysteine-rich domain homology
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-1436/Product: WC1 antigen #status predicted <MAT>
F:125-131/Domain: scavenger receptor cysteine-rich domain homology
F:132-234/Domain: scavenger receptor cysteine-rich domain homology <SR01>
F:236-340/Domain: scavenger receptor cysteine-rich domain homology <SR02>
F:373-476/Domain: scavenger receptor cysteine-rich domain homology <SR03>
F:478-581/Domain: scavenger receptor cysteine-rich domain homology <SR04>
F:583-686/Domain: scavenger receptor cysteine-rich domain homology <SR05>
F:687-789/Domain: scavenger receptor cysteine-rich domain homology <SR06>
F:791-895/Domain: scavenger receptor cysteine-rich domain homology <SR07>
F:928-1031/Domain: scavenger receptor cysteine-rich domain homology <SR08>
F:1033-1136/Domain: scavenger receptor cysteine-rich domain homology <SR10>
F:1152-1255/Domain: scavenger receptor cysteine-rich domain homology <SR11>

Query Match 82.2%; Score 37; DB 2; Length 1436;
Best Local Similarity 88.9%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
DB 6 HLSLRGLCV 14

RESULT 3
C75551
Glutamate synthase (NADH2) (EC 1.4.1.14) large chain DR0183 precursor [similarity] - Del
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Jun-2002
C:Accession: C75551
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75551
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1615 <W12>
A:Cross-references: GB:AE001980; GB:AE000513; NID:G6457844; PIDN:AAF09770.1; PID:G645783
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0183
A:Map position: 1
C:Superfamily: glutamate synthase (NADPH)
C:Keywords: 3Fe-4S; metalloprotein; oxidoreductase
F:1-52/Domain: propeptide #status predicted <PRO>
F:53-1615/Product: glutamate synthase #status predicted <MAT>
F:53/Active site: Cys #status predicted
F:1198,1204,1209/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 80.0%; Score 36; DB 2; Length 1615;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY -1 HLSLRGLF 8
DB 890 HMTLRGLF 897

RESULT 4
S20747
Gene X protein - hepatitis B virus (subtype ayw, patient C)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient C
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S20747

R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negat
A:Reference number: S20745
A:Accession: S20747
A:Molecule type: DNA
A:Residues: 1-66 <LAI>
A:Cross-references: EMBL:X65257; NID:G59429; PIDN:CAA46351.1; PID:G59432
A:Experimental source: subtype ayw, patient C
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 5
B48345
Gene X protein, truncated form - hepatitis B virus
C:Species: hepatitis B virus, HBV
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: B48345
R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert
Arch. Virol. 125, 299-304, 1992
A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer
A:Reference number: A48345; MUID:92352333; PMID:1642555
A:Accession: B48345
A:Molecule type: DNA
A:Residues: 1-134 <REP>
A:Cross-references: GB:IS41176; NID:G252541; PIDN:AAB22733.1; PID:G252542
A:Note: sequence extracted from NCBI backbone (NCBI:109914, NCBI:P:109915)
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
DB 52 HLSLRGL 58

RESULT 6
QOVLDI
Gene X protein - hepatitis B virus (subtype ayw)
C:Species: hepatitis B virus, HBV
C>Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994
C:Accession: A03719
R:Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.
Nature 281, 646-650, 1979
A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
A:Reference number: A93214; MUID:81012091; PMID:399327
A:Accession: A03719
A:Molecule type: DNA
A:Residues: 1-154 <GAL>
A:Cross-references: GB:J02203; GB:V01460
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7

Db 52 HLSLRGL 58
|||||

RESULT 7

QQVLBH
Gene X protein - hepatitis B virus (subtype ayw, strain PHB320)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, strain PHB320
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Jul-2000
C:Accession: A05237; S53144; S53173; S53195; S53210; S53217; S53222; S53224; S53235; S53280
R:Bickho, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
HEB Lett. 185, 208-212, 1985
A:Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A:Reference number: A05237; MUID:85204397; PMID:3996597
A:Accession: A05237
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <PIC>
A:Cross-references: EMBL:X02496; NID:G62280; PIDN:CA841697.1; PID:G4704317
A:Experimental source: subtype ayw, strain PHB320
R:Li, M.B.; Mazoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53144
A:Molecule type: DNA
A:Residues: 124-154 <LA2>
A:Cross-references: EMBL:X85267; NID:G736025; PIDN:CAA59548.1; PID:G736026; EMBL:X85284; S5305; EMBL:X85307; EMBL:X85308; EMBL:X85310; EMBL:X85312; EMBL:X85315; EMBL:X85317
A:Experimental source: isolate patient Pintus'85 et al.
A:Accession: S53173
A:Molecule type: DNA
A:Residues: 124-154 <LA2>
A:Cross-references: EMBL:X85277; NID:G736065; PIDN:CAA59575.1; PID:G736066
A:Experimental source: isolate patient Bio'90
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

RESULT 8

A48345
Gene X protein - hepatitis B virus
C:Species: hepatitis B virus, HBV
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: A48345
R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992
A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I
A:Reference number: A48345; MUID:92352333; PMID:1642555
A:Accession: A48345
A:Molecule type: DNA
A:Residues: 1-154 <REP>
A:Cross-references: GB:S41175; NID:G252539; PIDN:AAB22732.1; PID:G252540
A:Note: sequence extracted from NCBI backbone (NCBIN:109912, NCBI:P:109913)
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7

Db 52 HSLRGL 58
|||||

RESULT 9

QQVLAI
Gene X protein - hepatitis B virus (strain alpha1)
C:Species: hepatitis B virus, HBV
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: D34773
R:Tong, S.; Li, J.; Vitvitski, L.; Trepo, C.
Virology 176, 596-603, 1990
A:Title: Active hepatitis B virus replication in the presence of anti-HBe is associated
A:Reference number: A34773; MUID:90266476; PMID:2345966
A:Accession: D34773
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <TON>
A:Cross-references: EMBL:M32138; NID:G329667; PIDN:AAA45504.1; PID:G329671
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

RESULT 10

QQVLAW
Gene X protein - hepatitis B virus (subtype adw and adw2)
C:Species: hepatitis B virus, HBV
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C:Accession: A31289; B94409; A03719
R:Lo, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A:Title: Characteristics of the X gene of hepatitis B virus.
A:Reference number: A31289; MUID:89045656; PMID:3188399
A:Accession: A31289
A:Molecule type: DNA
A:Residues: 1-154 <LOS>
A:Experimental source: subtype adw
R:Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSLRGL 7
|||||

Db 52 HSLRGL 58

RESULT 11

QQVLKS
Gene X protein - hepatitis B virus (subtype adw, strain 991)
C:Species: hepatitis B virus, HBV
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S10380
R:Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.

submitted to the EMBL Data Library, February 1990

A;Reference number: S10380
A;Accession: S10380
A;Molecule type: DNA
A;Residues: 1-154 <KOE>
A;Cross-references: EMBL:X51970; NID:g1155012; PIDN:CAA36231.1; PID:g60432
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRGL 7
Db 52 HLSLRGL 58

RESULT 12

COVLCIP
gene X protein - hepatitis B virus (strain LSH, chimpanzee)
C;Species: hepatitis B virus, HBV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
A;Accession: D28885
R;Vaudin, M.; Molstenholme, A.J.; Tsiuaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
A;Reference number: A92796; M01D:86258473; PMID:2838576
A;Accession: D28885
A;Molecule type: DNA
A;Residues: 1-154 <VAU>
A;Cross-references: GB:D00220; NID:g221505; PIDN:BAA00160.1; PID:g221509
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRGL 7
Db 52 HLSLRGL 58

RESULT 13

S20756
gene X protein - hepatitis B virus (subtype ayw, patient E)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient E
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S20756
R;Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
submitted to the EMBL Data Library March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative

A;Reference number: S20745
A;Accession: S20756
A;Molecule type: DNA
A;Residues: 1-154 <LAI>
A;Cross-references: EMBL:X65259; NID:g59439; PIDN:CAA46360.1; PID:g59443
A;Experimental source: subtype ayw, patient E
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRGL 7
Db 52 HLSLRGL 58

RESULT 14

S47404
gene X protein - hepatitis B virus (subtype ayw4)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw4
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47404
R;Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isola
A;Reference number: S47404
A;Accession: S47404
A;Molecule type: DNA
A;Residues: 1-154 <PLU>
A;Cross-references: EMBL:Z35716; NID:g527435; PIDN:CAA84785.1; PID:g527436
A;Experimental source: subtype ayw4
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRGL 7
Db 52 HLSLRGL 58

RESULT 15

S47408
gene X protein - hepatitis B virus (subtype adw2)
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47408
R;Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isola
A;Reference number: S47408
A;Accession: S47408
A;Molecule type: DNA
A;Residues: 1-154 <PLU>
A;Cross-references: EMBL:Z35717; NID:g527440; PIDN:CAA84789.1; PID:g527441
A;Experimental source: subtype adw2
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 HLSLRGL 7
Db 52 HLSLRGL 58

Search completed: December 23, 2003, 08:41:04
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 25.8 seconds
(without alignments)
55.370 Million cell updates/sec

Title: US-09-989-621-1
Perfect score: 45
Sequence: 1 HSLRGLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	20	AAV24459
2	37	82.2	1436	23	ABJ09377
3	35	77.8	8	23	ABJ07083
4	35	77.8	9	15	AAV52005
5	35	77.8	9	23	ABJ06063
6	35	77.8	9	23	ABJ06091
7	35	77.8	9	23	ABJ07228
8	35	77.8	9	23	ABJ07543
9	35	77.8	9	23	ABJ07543

10	35	77.8	9	23	ABJ09365	Hepatitis B virus
11	35	77.8	9	23	ABJ09377	Hepatitis B virus
12	35	77.8	10	23	ABJ07083	Hepatitis B virus
13	35	77.8	11	23	ABJ06064	Hepatitis B virus
14	35	77.8	11	23	ABJ06092	Hepatitis B virus
15	35	77.8	11	23	ABJ07119	Hepatitis B virus
16	35	77.8	11	23	ABJ07342	Hepatitis B virus
17	35	77.8	11	23	ABJ07764	Hepatitis B virus
18	35	77.8	11	23	ABJ08017	Hepatitis B virus
19	35	77.8	15	19	AAV85245	Helper T-cell pept
20	35	77.8	15	19	AAV85248	Helper T-cell pept
21	35	77.8	15	23	ABJ08950	Hepatitis B virus
22	35	77.8	15	23	ABJ08957	Hepatitis B virus
23	35	77.8	15	23	ABJ09242	Hepatitis B virus
24	35	77.8	15	23	ABJ09249	Hepatitis B virus
25	35	77.8	15	23	ABJ09371	Hepatitis B virus
26	35	77.8	15	23	ABJ09383	Hepatitis B virus
27	35	77.8	15	23	ABJ09387	Hepatitis B virus
28	35	77.8	134	16	AAV71563	Hepatitis B virus
29	35	77.8	146	22	AAV66920	HBV HBx protein.
30	35	77.8	153	22	AAV04712	Hepatitis B virus
31	35	77.8	154	6	AAV50461	Sequence of the an
32	35	77.8	154	9	AAV82174	Peptide encoded by
33	35	77.8	154	21	AAV58473	Hepatitis B virus
34	35	77.8	154	21	AAV54047	Amino acid sequenc
35	35	77.8	154	21	AAV44351	Human hepatitis B
36	34	75.6	25	23	ABG62234	Eubacterial DNA Po
37	34	75.6	124	22	AAU46748	Propionibacterium
38	33	73.3	50	22	AAU58277	Propionibacterium
39	33	73.3	144	22	AAU61791	Novel human secret
40	33	73.3	200	22	AAU31252	Human prostate can
41	33	73.3	224	21	AAV56959	Amino acid sequenc
42	33	73.3	256	22	AAV68037	Human AOP-1 protei
43	33	73.3	256	23	ABP53042	Streptococcus poly
44	33	73.3	510	23	ABP27669	Beta, Beta-caroten
45	33	73.3	526	21	AAV97311	

ALIGNMENTS

RESULT 1	AAV24459	AAV24459
ID	AAV24459	standard; peptide; 9 AA.
AC	AAV24459;	
DT	23-SEP-1999	(first entry)
DE	Hepatitis B virus X protein peptide #1.	
KW	Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;	
KW	CTL; antigen; immunity; liver cancer.	
OS	Hepatitis B virus.	
OS	Synthetic.	
PN	WO9936434-A1.	
DD	22-JUL-1999.	
PF	19-JAN-1998;	98WO-KR00010.
PR	19-JAN-1998;	98WO-KR00010.
PA	(MOGA-) MOGAM BIOTECHNOLOGY RES INST.	
PI	Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;	
PI	Lee K;	
DR	WPI; 1999-444387/37.	
PT	Hepatitis B virus protein X-derived peptide antigens used to	

PT stimulate cytotoxic T lymphocytes, useful for treatment of
 PT HBV-associated diseases, especially liver cancer
 XX
 PS Claim 1; Page 24; 33pp; English.
 XX
 CC The present invention describes peptide antigens AAY24459 to AAY24463
 CC derived from the X protein of hepatitis B virus (HBV) which are
 CC recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CC derived from HBV X protein are useful for inducing CTLs against the
 CC virus or inducing immunological tolerance to the virus. pH-sensitive
 CC liposomes containing the peptide antigens are used to induce cellular
 CC immunity so that CTLs specific to the virus can be produced. This is
 CC useful for prevention and treatment of HBV-associated diseases,
 CC especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CC the selective transportation of anti-cancer drugs.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 45; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLSLRGLFV 9
 DB 1 HLSLRGLFV 9
 RESULT 2
 AAB66098
 ID AAB66098 standard; Protein; 1436 AA.
 XX
 AC AAB66098;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE Bovine WC1 protein.
 XX
 KW Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder;
 KW central nervous system; focal brain disorder; bipolar affective disorder;
 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;
 KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;
 KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
 KW neuropsychiatric; psychoactive substance use; anxiety.
 XX
 OS Bos sp.
 XX
 PN WO200077239-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14858.
 XX
 PR 14-JUN-1999; 99US-0333159.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 FI McCarthy SA, Fraser CC, Sharp JD, Barnes TW;
 XX
 DR WPI; 2001-032313/04.
 DR N-PSDB; AAF45141.
 XX
 PT TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for
 PT screening assays and diagnostic assays and for the treatment of
 PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's
 PT disease -
 XX
 PS Disclosure; Fig 2; 359pp; English.
 XX
 CC The present invention relates to TANGO or INTERCEPT proteins and coding
 CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,
 CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding
 CC sequences are useful for the treatment of neurological disorders such as
 CC central nervous system (CNS) disorders, CNS-related disorders, focal

CC brain disorders, global-diffuse cerebral disorders and other
 CC neurological and cerebrovascular disorders. The CNS disorders include
 CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
 CC lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,
 CC autonomic function disorders such as hypertension and sleep disorders,
 CC neuropsychiatric disorders, psychoactive substance use disorders,
 CC anxiety, and bipolar affective disorder. The present sequence is a
 CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT
 CC sequences of the present invention.
 XX
 SQ Sequence 1436 AA;
 Query Match 82.2%; Score 37; DB 22; Length 1436;
 Best Local Similarity 88.9%; Pred. No. 72;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HLSLRGLFV 9
 DB 6 HLSLRGLCV 14
 RESULT 3
 ABJ07014
 ID ABJ07014 standard; Peptide; 8 AA.
 XX
 AC ABJ07014;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus epitope #1232.
 XX
 KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200219986-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000WO-US24802.
 XX
 PR 08-SEP-2000; 2000WO-US24802.
 XX
 PA (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTE A.
 XX
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/59.
 XX
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX
 PS Disclosure; Page 134; 228pp; English.
 XX
 CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 8 AA;
 Query Match 77.8%; Score 35; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLSLRGL 7
 DB 2 HLSLRGL 8

```

RESULT 4
AAR59205
ID AAR59205 standard; peptide; 9 AA.
XX AC AAR59205;
XX AC AAR59205;
XX DT 25-MAR-2003 (updated)
XX DT 03-MAY-1995 (first entry)
XX DE Peptide fragment (1.0212) of HBV binds HLA-A2.1.
XX KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVc; EBV;
XX KW HIV1; core antigen; surface antigen; pharmaceutical composition;
XX KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
XX KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
XX KW human leukocyte antigen.
XX OS Hepatitis B Virus adr.
XX PN WO9420127-A1.
XX PD 15-SEP-1994.
XX PF 04-MAR-1994; 94WO-US02353.
XX PR 05-MAR-1993; 93US-0027146.
XX PR 04-JUN-1993; 93US-0073205.
XX PR 29-NOV-1993; 93US-0159184.
XX (CYTE-) CYTEL CORP.
XX PA Grey HM, Kast WM, Sette A, Sidney J;
XX PI WPI; 1994-302678/37.
XX DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
XX PT for treatment or prophylaxis of cancer, virus infection or
XX PT autoimmune diseases.
XX PS Example 5; Page 104; 138pp; English.
XX CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
XX binding motif. These peptides bind HLA-A2.1 and have a binding affinity
XX of at least 1% as compared to a reference peptide (AAR71293). AAR59205
XX has an IC50 of 0.0004 and the sequence occurs at position 1470 in the HBV
XX "X" protein (as given in the specification). The peptides of the
XX invention can induce cytotoxic T lymphocytes which can react with target
XX cells. They can be used for the treatment or prophylaxis of cancer, eg.
XX CC prostate cancer or lymphoma, etc.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 9 AA;
XX Query Match 77.8%; Score 35; DB 15; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 HLSLRGL 7
XX Db 1 HLSLRGL 7
XX RESULT 6
XX ABJ06063
XX ID ABJ06063 standard; Peptide; 9 AA.
XX AC ABJ06063;
XX DT 14-NOV-2002 (first entry)
XX DE Hepatitis B virus epitope #281.
XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
XX KW virucide; hepatotropic; antiinflammatory.
XX OS Hepatitis B virus.
XX PN WO200219986-A1.
XX PD 14-MAR-2002.
XX PF 08-SEP-2000; 2000WO-US24802.
XX PR 08-SEP-2000; 2000WO-US24802.
XX PA (EPIM-) EPIMMUNE INC.
XX PA (SETT/) SETTE A.
XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
XX PI Celis E, Kubo RT, Grey HM, Chesnut RW;
XX DR WPI; 2002-643192/69.
XX
XX HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I;
XX major histocompatibility complex; immunomodulator.
XX OS Hepatitis B virus.
XX PN KR98022440-A.
XX PD 06-JUL-1998.
XX PF 23-SEP-1996; 96KR-0041612.
XX PR 23-SEP-1996; 96KR-0041612.
XX PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX PI Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;
XX WPI; 1999-300977/25.
XX Synthetic peptide having immunoregulating activities for hepatitis B
XX virus -
XX PS Example 1; Page 4; 7pp; Korean.
XX CC The invention relates to peptides derived from the hepatitis B virus
XX (HBV) X protein (AAM52970-AAM52973). The peptides are presented on major
XX histocompatibility complex (MHC) class I molecules and act as cytotoxic
XX T-lymphocyte (CTL) epitopes. Sequences AAM52974-AAM52984 represent HBV
XX X protein-derived peptides used in an exemplification of the invention.
XX SQ Sequence 9 AA;
XX Query Match 77.8%; Score 35; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 HLSLRGL 7
XX Db 1 HLSLRGL 7
XX RESULT 5
XX AAM52978
XX ID AAM52978 standard; peptide; 9 AA.
XX AC AAM52978;
XX DT 12-MAR-2002 (first entry)
XX DE Hepatitis B virus X protein peptide (residues 52-60).

```


PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -

PS Disclosure; Page 115; 228pp; English.

CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 9 AA;

Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 |||||
 Db 3 HLSLRGL 9

RESULT 7
 ABJ06091
 ID ABJ06091 standard; Peptide; 9 AA.

XX AC ABJ06091;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #309.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX FN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US24802.

XX PR 08-SEP-2000; 2000WO-US24802.

XX PA (EPIM-) EPIMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;
 XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -

PS Disclosure; Page 115; 228pp; English.

CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 9 AA;

Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7

Db 1 HLSLRGL 7
 |||||

RESULT 8

ABJ07228
 ID ABJ07228 standard; Peptide; 9 AA.

XX AC ABJ07228;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #1446.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX FN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US24802.

XX PR 08-SEP-2000; 2000WO-US24802.

XX PA (EPIM-) EPIMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;
 XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -

PS Disclosure; Page 138; 228pp; English.

XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 9 AA;

Query Match 77.8%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 |||||
 Db 3 HLSLRGL 9

RESULT 9

ABJ07543
 ID ABJ07543 standard; Peptide; 9 AA.

XX AC ABJ07543;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #1761.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 XX virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

```

PN WO200219986-A1.
PD 14-MAR-2002.
XX
XX
XX 08-SEP-2000; 2000WO-US24802.
XX
XX 08-SEP-2000; 2000WO-US24802.
XX
XX (EPIM-) EPIMUNE INC.
PA (SETT/) SETTE A.
XX
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Celis E, Kubo RT, Grey HM, Chestnut RW;
XX
XX WPI; 2002-643192/69.
XX
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -
XX
XX Disclosure; Page 146; 228pp; English.
XX
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 77.8%; Score 35; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HLSLRGL 7
XX Db 2 HLSLRGL 8
XX
XX RESULT 11
XX ABJ09377
XX ID ABJ09377 standard; Peptide; 9 AA.
XX
XX AC ABJ09377;
XX
XX DT 14-NOV-2002 (first entry)
XX
XX DE Hepatitis B virus epitope #3565.
XX
XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
XX virucide; hepatotropic; antiinflammatory.
XX
XX OS Hepatitis B virus.
XX
XX PN WO200219986-A1.
XX
XX PD 14-MAR-2002.
XX
XX PF 08-SEP-2000; 2000WO-US24802.
XX
XX PR 08-SEP-2000; 2000WO-US24802.
XX
XX PA (EPIM-) EPIMUNE INC.
XX (SETT/) SETTE A.
XX
XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
XX Celis E, Kubo RT, Grey HM, Chestnut RW;
XX
XX DR WPI; 2002-643192/69.
XX
XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
XX infection, and/or for stimulating an immune response to HBV, comprises
XX a HBV peptide epitope -
XX
XX Disclosure; Page 186; 228pp; English.
XX
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 77.8%; Score 35; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HLSLRGL 7
XX Db 2 HLSLRGL 8
XX
XX RESULT 10
XX ABJ09365
XX ID ABJ09365 standard; Peptide; 9 AA.
XX
XX AC ABJ09365;
XX
XX DT 14-NOV-2002 (first entry)
XX
XX DE Hepatitis B virus epitope #3553.
XX
XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
XX virucide; hepatotropic; antiinflammatory.
XX
XX OS Hepatitis B virus.
XX
XX PN WO200219986-A1.
XX
XX PD 14-MAR-2002.
XX
XX PF 08-SEP-2000; 2000WO-US24802.
XX
XX PR 08-SEP-2000; 2000WO-US24802.
XX
XX PA (EPIM-) EPIMUNE INC.
XX (SETT/) SETTE A.
XX
XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
XX Celis E, Kubo RT, Grey HM, Chestnut RW;
XX
XX DR WPI; 2002-643192/69.
XX
XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
XX infection, and/or for stimulating an immune response to HBV, comprises
XX a HBV peptide epitope -

```


CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

XX
 XX Sequence 11 AA;

Query Match 77.8%; Score 35; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred.No. 0.99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 |||||
 Db 1 HLSLRGL 7

RESULT 15

AEJ07119
 ID ABJ07119 standard; Peptide; 11 AA.

XX
 AC ABJ07119;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #1337.

KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

XX WO200219986-A1.

PN 14-MAR-2002.

PD 08-SEP-2000; 2000WO-US24802.

PF 08-SEP-2000; 2000WO-US24802.

PR (EPIM-) EPIMUNE INC.

PA (SETT/) SETTE A.

PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;

PI Celis E, Kubo RT, Grey HW, Chesnut RW;

XX WPI; 2002-643192/69.

DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -

XX Disclosure; Page 136; 228pp; English.

XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.

XX Sequence 11 AA;

Query Match 77.8%; Score 35; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred.No. 0.99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRGL 7
 |||||
 Db 5 HLSLRGL 11

Search completed: December 23, 2003, 08:43:59
 Job time : 27.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:41:18 ; Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

Title: US-09-989-621-1
Perfect score: 45
Sequence: 1 HSLRGLFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	4	US-09-051-006-1
2	36	80.0	322	4	US-09-328-352-5489
3	35	77.8	15	4	US-09-009-953-147
4	35	77.8	15	4	US-09-009-953-150
5	35	77.8	19	6	5183734-6
6	35	77.8	20	6	5183734-14
7	35	77.8	153	6	5196194-20
8	35	77.8	153	6	5204446-4
9	35	77.8	154	4	US-09-719-528A-5
10	35	77.8	154	6	5183734-1
11	32	71.1	180	4	US-08-913-159-13
12	32	71.1	377	1	US-07-959-946-1
13	32	71.1	377	1	US-08-333-577-1
14	32	71.1	377	5	PCT-US92-08634-1
15	32	71.1	4536	4	US-09-180-422B-27
16	32	71.1	4563	1	US-09-108-006C-1
17	31	68.9	201	1	US-08-415-751-2
18	31	68.9	257	2	US-08-467-265-16
19	31	68.9	257	3	US-08-467-265-16
20	31	68.9	257	3	US-09-407-891-16
21	31	68.9	308	4	US-09-252-991A-30126
22	31	68.9	351	1	US-08-415-751-17
23	31	68.9	440	4	US-09-077-955-26
24	31	68.9	456	4	US-09-077-955-25
25	31	68.9	492	2	US-08-644-271-32
26	31	68.9	492	4	US-09-077-955-36
27	31	68.9	530	4	US-09-252-991A-23666

28	31	68.9	1156	3	US-08-996-083-1	Sequence 1, Appli
29	31	68.9	1156	3	US-09-429-516-1	Sequence 1, Appli
30	31	68.9	1156	3	US-09-429-516-3	Sequence 3, Appli
31	30	66.7	199	1	US-08-299-162A-2	Sequence 2, Appli
32	30	66.7	199	2	US-08-467-265-14	Sequence 14, Appli
33	30	66.7	199	2	US-08-467-265-17	Sequence 17, Appli
34	30	66.7	199	3	US-08-467-265-14	Sequence 14, Appli
35	30	66.7	199	3	US-08-467-265-17	Sequence 17, Appli
36	30	66.7	199	3	US-09-407-891-14	Sequence 14, Appli
37	30	66.7	199	3	US-09-407-891-17	Sequence 17, Appli
38	30	66.7	371	4	US-09-252-991A-27127	Sequence 27127, A
39	30	66.7	482	4	US-09-252-991A-20932	Sequence 20932, A
40	30	66.7	553	3	US-08-845-546-12	Sequence 12, Appli
41	30	66.7	708	4	US-09-328-352-6131	Sequence 6131, Ap
42	30	66.7	719	4	US-09-252-991A-28768	Sequence 28768, A
43	30	66.7	746	4	US-09-252-991A-29228	Sequence 29228, A
44	29	64.4	13	4	US-09-461-325-525	Sequence 525, App
45	29	64.4	43	4	US-09-227-357-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-09-051-006-1
; Sequence 1, Application US/09051006
; Patent No. 6380353
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/03154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-1

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSLRGLFV 9
| | | | |
DB 1 HSLRGLFV 9

RESULT 2

US-09-328-352-5489
; Sequence 5489, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANN FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5489
; LENGTH: 322
; TYPE: PRT

ORGANISM: Acinetobacter baumannii
us-09-328-352-5489

Query Match 80.0%; Score 36; DB 4; Length 322;
Best Local Similarity 55.6%; Pred. No. 5.5,
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
Db 7 HIKLRGIFI 15

RESULT 3

us-09-009-953-147

Sequence 147, Application US/09009953

Patent No. 6413517

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

TITLE OF INVENTION: Identification of Broadly

Reactive DR Restricted Epitopes

CORRESPONDENCE ADDRESS: 274

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 147:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 147:

us-09-009-953-147

Query Match 77.8%; Score 35; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7

Db 3 HLSLRGL 9

RESULT 4

us-09-009-953-150

Sequence 150, Application US/09009953

Patent No. 6413517

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

TITLE OF INVENTION: Identification of Broadly

Reactive DR Restricted Epitopes

CORRESPONDENCE ADDRESS: 274

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 147:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 147:

us-09-009-953-150

Query Match 77.8%; Score 35; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7

Db 3 HLSLRGL 9

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

TITLE OF INVENTION: Identification of Broadly

Reactive DR Restricted Epitopes

CORRESPONDENCE ADDRESS: 274

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 150:

us-09-009-953-150

Query Match 77.8%; Score 35; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7

Db 1 HLSLRGL 7

RESULT 5

5183734-6

Patent No. 5183734

APPLICANT: MORIARTY, ANN M.

TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

FOR ASSAYING SV40 HBXAG

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,982

FILING DATE: 17-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 54,424

FILING DATE: 26-MAY-1987

APPLICATION NUMBER: 648,142

FILING DATE: 07-SEP-1984

APPLICATION NUMBER: 587,570

FILING DATE: 08-MAR-1984

SEQ ID NO: 6

LENGTH: 19

5183734-6

Query Match 77.8%; Score 35; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRL 7
|||
Db 10 HLSLRL 16

RESULT 6
5183734-14
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:14:
; LENGTH: 20
5183734-14

Query Match 77.8%; Score 35; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRL 7
|||
Db 11 HLSLRL 17

RESULT 7
5196194-20
; Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:20:
; LENGTH: 153
5196194-20

Query Match 77.8%; Score 35; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRL 7
|||
Db 52 HLSLRL 58

RESULT 8
5204446-4
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI; OSANAI, MASATOSHI

; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:4:
; LENGTH: 153
5204446-4

Query Match 77.8%; Score 35; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRL 7
|||
Db 52 HLSLRL 58

RESULT 9
US-09-719-528A-5
; Sequence 5, Application US/09719528A
; Patent No. 6558675
; GENERAL INFORMATION:
; APPLICANT: Oom, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-719-528A-5

Query Match 77.8%; Score 35; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSLRL 7
|||
Db 52 HLSLRL 58

RESULT 10
 5183734-1
 ; PATENT NO. 5183734
 ; APPLICANT: MORIARTY, ANN M.
 ; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
 ; FOR ASSAYING SV40 HBXAG
 ; NUMBER OF SEQUENCES: 17
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/553,982
 ; FILING DATE: 17-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 54,424
 ; FILING DATE: 24-MAY-1987
 ; APPLICATION NUMBER: 648,142
 ; FILING DATE: 07-SEP-1984
 ; APPLICATION NUMBER: 587,570
 ; FILING DATE: 08-MAR-1984
 ; SEQ ID NO:1
 ; LENGTH: 154
 5183734-1

Query Match 77.8%; Score 35; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7
 Db 52 HLSLRGL 58

RESULT 11
 US-08-913-159-13
 ; Sequence 13, Application US/08913159
 ; Patent No. 6300109
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Plasmid-derived type II
 ; TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
 ; NUMBER OF SEQUENCES: 14
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (BFO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/913,159
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 0179/95
 ; FILING DATE: 17-FEB-1995
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 180 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-913-159-13

Query Match 71.4%; Score 32; DB 4; Length 180;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
 Db 148 HVSLSLFLV 156

RESULT 12
 US-07-959-946-1
 ; Sequence 1, Application US/07959946
 ; Patent No. 5408038
 ; GENERAL INFORMATION:

APPLICANT: Smith, Richard K.
 APPLICANT: Koduri, Raju
 APPLICANT: Young, Stephen G.
 APPLICANT: Witzum, Joseph L.
 APPLICANT: Curtiss, Linda K.
 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Goldsmith, Shore, Sukter &
 ADDRESSEE: Milnamow, Ltd.
 STREET: 180 No. 5408038th Stetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/959,946
 FILING DATE: 19921008
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,706
 FILING DATE: 18-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Ganson, Edward P.
 REGISTRATION NUMBER: 29,381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5400
 TELEFAX: (312) 616-5460
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 377 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-959-946-1

Query Match 71.1%; Score 32; DB 1; Length 377;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HLSLRGLF 8
 Db 330 HLQLEGLF 337

RESULT 13
 US-08-333-577-1
 ; Sequence 1, Application US/08333577
 ; Patent No. 5786206
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Richard K.
 ; APPLICANT: Koduri, Raju
 ; APPLICANT: Young, Stephen G.
 ; APPLICANT: Witzum, Joseph L.
 ; APPLICANT: Curtiss, Linda K.
 ; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 ; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Goldsmith, Shore, Sukter &
 ; ADDRESSEE: Milnamow, Ltd.
 ; STREET: 180 No. 5786206th Stetson, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acids
MOLECULE TYPE: protein
US-08-333-577-1

Query Match 71.1%; Score 32; DB 1; Length 377;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
DB 330 HLQLEGLF 337

RESULT 14
PCT-US92-08634-1
Sequence 1, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnarcw, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: Protein
PCT-US92-08634-1

Query Match 71.1%; Score 32; DB 5; Length 377;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
DB 330 HLQLEGLF 337

RESULT 15
US-180-422B-27
Sequence 27, Application US/09180422B
Patent No. 644644
GENERAL INFORMATION:
APPLICANT: BRUCKDORFER, KARL R
ETTELAIE, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPOPROTEIN B-100
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27

Query Match 71.1%; Score 32; DB 4; Length 4536;
Best Local Similarity 75.0%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
DB 3543 HLQLEGLF 3550

Search completed: December 23, 2003, 08:53:45
Job time : 11.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
(without alignments)
21.169 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HLSRLGLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	10	US-09-989-621-1
2	37	82.2	1436	11	US-09-759-1303-448
3	37	82.2	1436	14	US-10-042-431-78
4	35	77.8	154	15	US-10-029-264-5
5	33	73.3	224	10	US-09-925-300-1537
6	33	73.3	256	12	US-10-408-766-23
7	33	73.3	526	15	US-10-053-192-1
8	33	73.3	864	12	US-10-238-075-395
9	32	71.1	430	9	US-09-741-669-442
10	32	71.1	1871	12	US-10-144-194A-114
11	32	71.1	1906	12	US-10-144-194A-88
12	32	71.1	4563	10	US-09-870-759-128
13	32	71.1	4563	11	US-09-802-640-32
14	32	71.1	4563	12	US-09-751-708A-128
15	31	68.9	53	12	US-10-029-386-31587

Sequence 787, App
Sequence 787, App
Sequence 10, Appl
Sequence 16, Appl
Sequence 21, Appl
Sequence 26, Appl
Sequence 25, Appl
Sequence 36, Appl
Sequence 14772, A
Sequence 1, Appl
Sequence 1076, Ap
Sequence 100, App
Sequence 13, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 53, Appl
Sequence 973, App
Sequence 10964, A
Sequence 46, Appl
Sequence 4, Appl
Sequence 3253, Ap
Sequence 520, App
Sequence 11180, A
Sequence 525, App
Sequence 264, App
Sequence 5482, Ap
Sequence 4907, Ap
Sequence 328, App
Sequence 3068, Ap

74 US-09-764-869-787
74 US-10-091-504-787
15 US-09-946-290-10
12 US-09-911-346-16
257 10 US-10-408-766-21
257 12 US-10-016-283-26
440 14 US-10-016-283-25
456 14 US-10-016-283-36
492 14 US-10-156-761-14772
616 15 US-09-757-716-1
1156 9 US-09-764-869-1076
66 9 US-10-091-504-1076
66 15 US-09-895-298-100
131 11 US-09-202-329-13
198 11 US-09-911-346-14
199 10 US-09-911-346-17
199 10 US-10-205-194-53
233 9 US-09-925-301-973
237 9 US-09-815-242-10964
237 15 US-10-260-877-46
506 15 US-10-053-192-4
552 12 US-10-094-749-3253
553 15 US-10-225-567A-520
1709 15 US-10-156-761-11180
13 15 US-10-012-542-525
43 11 US-09-983-802-264
53 15 US-10-106-698-5482
103 11 US-09-764-891-4907
110 9 US-09-867-550-328
128 15 US-10-128-714-3068

ALIGNMENTS

RESULT 1
US-09-989-621-1
Sequence 1, Application US/09989621
Patent No. US20030151683A1
GENERAL INFORMATION:
APPLICANT: Mogam Biotechnology Research Institute
APPLICANT: Kim, Tae-Young
APPLICANT: Lee, Ki-Young
APPLICANT: Chang, Jin-Soo
APPLICANT: Cho, Sung-Yoo
APPLICANT: Hwang, Yu-Kyeong
APPLICANT: Choi, Myeong
APPLICANT: Cheong, Hong-Seok
TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
FILE REFERENCE: 0136/08154
CURRENT APPLICATION NUMBER: US/09/989, 621
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/051,006
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-989-621-1

Query Match 100.0%; Score 45; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSRLGLFV 9

DB 1 HLSRLGLFV 9

RESULT 2

US-09-759-130B-448
; Sequence 448, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-5350MIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Bovine
US-09-759-130B-448

Query Match 82.2%; Score 37; DB 11; Length 1436;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
| | | | |
Db 6 HLSLRGLCV 14

RESULT 3
US-10-042-431-78
; Sequence 78, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-612
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25

US-09-333-159
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Bos sp.
US-10-042-431-78

Query Match 82.2%; Score 37; DB 14; Length 1436;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLSLRGLFV 9
| | | | |
Db 6 HLSLRGLCV 14

RESULT 4
US-10-209-264-5
; Sequence 5, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/209,264
; FILING DATE: 31-Jul-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SG98/00046
; FILING DATE: 19-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-013109-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-209-264-5

Query Match 77.8%; Score 35; DB 15; Length 154;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLSLRGL 7
| | | | |

Db 52 HSLRLCL 58

RESULT 5

US-09-925-300-1537
 ; Sequence 1537, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1537
 ; LENGTH: 224
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-300-1537

Query Match 73.3%; Score 33; DB 10; Length 224;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9

Db 149 LALRGLFI 156

RESULT 6

US-10-408-766-23
 ; Sequence 23, Application US/10408766
 ; Publication No. US20030228294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wensev, Diane
 ; APPLICANT: Dang, Chi
 ; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH VIA
 ; FILE REFERENCE: PEROXIREDOXIN 3
 ; CURRENT APPLICATION NUMBER: US/10/408,766
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/370,873
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-766-23

Query Match 73.3%; Score 33; DB 12; Length 256;
 Best Local Similarity 75.0%; Pred. No. 81;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9

Db 181 LALRGLFI 188

RESULT 7

US-10-053-192-1
 ; Sequence 1, Application US/10053192
 ; Publication No. US20030087336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BACHMANN, Heinrich
 ; APPLICANT: BRUGGER, Roland

; APPLICANT: FRIEDLEIN, Arno M
 ; APPLICANT: WIRTZ, Gabriele M
 ; APPLICANT: WOGGON, Wolf-Dietrich
 ; APPLICANT: WYSS, Adrian
 ; APPLICANT: WYSS, Markus
 ; TITLE OF INVENTION: BETA,BETA-CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID
 ; FILE REFERENCE: SEQUENCES CODING THEREFOR AND THEIR USE
 ; CURRENT APPLICATION NUMBER: US/10/053,192
 ; CURRENT FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 103382.0
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 526
 ; TYPE: PRT
 ; ORGANISM: CHICKEN
 US-10-053-192-1

Query Match 73.3%; Score 33; DB 15; Length 526;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HSLRGLFV 9

Db 508 HLDLRGNFI 516

RESULT 8

US-10-238-075-395
 ; Sequence 395, Application US/10238075
 ; Publication No. US20030148324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: I.N.S.E.R.M.
 ; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
 ; FILE REFERENCE: BLANDINE
 ; CURRENT APPLICATION NUMBER: US/10/238,075
 ; CURRENT FILING DATE: 2002-09-10
 ; PRIOR APPLICATION NUMBER: 0003145
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 1576
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 395
 ; LENGTH: 864
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-10-238-075-395

Query Match 73.3%; Score 33; DB 12; Length 864;
 Best Local Similarity 62.5%; Pred. No. 3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSLRGLF 8

Db 776 HIGIRGLF 783

RESULT 9

US-09-741-669-442
 ; Sequence 442, Application US/09741669
 ; Patent No. US20030022718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Forsyth, R. Allyn
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; TITLE OF INVENTION: Genes identified as required for
 ; FILE REFERENCE: proliferation of E. coli
 ; CURRENT APPLICATION NUMBER: ELITRA.009A
 ; CURRENT FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US/09/741,669
 ; PRIOR APPLICATION NUMBER: US 60/173005

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; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 442
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-442

Query Match 71.1%; Score 32; DB 9; Length 430;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
| | | | |
Db 151 HLSLRGIV 159

RESULT 10
US-10-144-194A-114
; Sequence 114, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 1871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-114

Query Match 71.1%; Score 32; DB 12; Length 1871;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
| | | | |
Db 342 HLSLRPIFL 350

RESULT 11
US-10-144-194A-88
; Sequence 88, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 1906
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-88

Query Match 71.1%; Score 32; DB 12; Length 1906;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
| | | | |
Db 377 HLSLRPIFL 385

RESULT 12
US-10-144-194A-114
; Sequence 114, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 1871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-114

Query Match 71.1%; Score 32; DB 12; Length 1871;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLSLRGLFV 9
| | | | |
Db 342 HLSLRPIFL 350

RESULT 13
US-09-802-640-32
; Sequence 32, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsel Aruna
; APPLICANT: Klevy Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-32

Query Match 71.1%; Score 32; DB 11; Length 4563;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLSLRGLF 8
| | | | |
Db 3570 HQLQGLF 3577

RESULT 14
US-09-751-708A-128
; Sequence 128, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: Tervan, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128

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; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-706A-128

Query Match      71.1%; Score 32; DB 12; Length 4563;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 HLSLRGLF 8
      |||||
Db      3570 HLCLEGLF 3577

RESULT 15
US-10-029-386-31587
; Sequence 31587, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEONICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31587
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008985.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
; OTHER INFORMATION: SWISSPROT HIT: Q54513, EVALUE 6.20e+00
US-10-029-386-31587

Query Match      68.9%; Score 31; DB 12; Length 53;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HLSLRGL 7
      |||||
Db      28 HLELRGL 34

Search completed: December 23, 2003, 08:52:48
Job time : 80.4 secs
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GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 CM protein - protein search, using sw model
 Run on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
 (without alignments)
 21.169 Million cell updates/sec

Title: US-09-989-621-2
 Perfect score: 45
 Sequence: 1 VLHRTGL 9
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
 3: /cgn2_6/ptodata/1/pubaa/US05_NEW_PUB.pep.*
 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
 9: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
 10: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
 12: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
 17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
 18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	10	US-09-989-621-2
2	39	86.7	154	15	US-10-209-264-5
3	34	75.6	293	12	US-10-427-442-12
4	34	75.6	691	12	US-10-258-165-254
5	33	73.3	630	11	US-09-938-795A-1
6	32	71.1	403	15	US-10-156-761-10822
7	32	71.1	448	9	US-09-815-242-10596
8	32	71.1	748	9	US-09-815-242-10278
9	32	71.1	869	9	US-09-815-242-13880
10	32	71.1	869	9	US-09-815-242-5230
11	32	71.1	882	9	US-09-815-242-12526
12	31	68.9	23	14	US-10-001-870-215
13	31	68.9	65	15	US-10-050-704-148
14	31	68.9	37	15	US-10-050-704-307
15	31	68.9	320	9	US-09-872-153-22

16	31	68.9	320	16	US-10-176-306-20	Sequence 20, Appl
17	31	68.9	369	12	US-09-954-342-8	Sequence 8, Appl
18	31	68.9	369	12	US-09-954-342-12	Sequence 12, Appl
19	31	68.9	390	12	US-09-944-049-20	Sequence 20, Appl
20	31	68.9	412	12	US-09-944-049-22	Sequence 22, Appl
21	31	68.9	422	12	US-09-954-342-10	Sequence 10, Appl
22	31	68.9	424	10	US-09-843-905A-13	Sequence 13, Appl
23	31	68.9	424	12	US-10-317-250-13	Sequence 13, Appl
24	31	68.9	483	12	US-10-029-386-32939	Sequence 32939, A
25	31	68.9	734	15	US-10-054-683-19	Sequence 19, Appl
26	31	68.9	734	15	US-10-205-823-10	Sequence 10, Appl
27	31	68.9	735	15	US-10-205-823-8	Sequence 8, Appl
28	31	68.9	753	15	US-10-205-823-6	Sequence 6, Appl
29	30	66.7	84	12	US-10-340-578-54	Sequence 54, Appl
30	30	66.7	239	14	US-10-076-785-36	Sequence 36, Appl
31	30	66.7	265	11	US-09-866-050A-655	Sequence 655, App
32	30	66.7	303	9	US-09-765-272-202	Sequence 202, App
33	30	66.7	328	12	US-09-769-744A-48	Sequence 48, Appl
34	30	66.7	340	9	US-09-815-342-10736	Sequence 10736, A
35	30	66.7	376	10	US-09-882-872-2	Sequence 2, Appl
36	30	66.7	414	12	US-10-063-735-102	Sequence 102, App
37	30	66.7	414	12	US-10-199-672-314	Sequence 314, App
38	30	66.7	414	12	US-10-187-749-314	Sequence 314, App
39	30	66.7	414	12	US-10-194-457-314	Sequence 314, App
40	30	66.7	414	12	US-10-184-642-314	Sequence 314, App
41	30	66.7	414	12	US-10-196-747-314	Sequence 314, App
42	30	66.7	414	12	US-10-173-689-314	Sequence 314, App
43	30	66.7	414	12	US-10-173-690-314	Sequence 314, App
44	30	66.7	414	12	US-10-173-691-314	Sequence 314, App
45	30	66.7	414	12	US-10-173-692-314	Sequence 314, App

ALIGNMENTS

RESULT 1

US-09-989-621-2
 ; Sequence 2, Application US/09989621
 ; Patent No. US20020151683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mogam Biotechnology Research Institute
 ; APPLICANT: Kim, Tae-Young
 ; APPLICANT: Lee, Ki-Young
 ; APPLICANT: Chang, Jin-Soo
 ; APPLICANT: Cho, Sung-Yoo
 ; APPLICANT: Hwang, Yu-Kyeong
 ; APPLICANT: Choi, Myeong
 ; APPLICANT: Cheong, Hong-Seok
 ; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
 ; FILE REFERENCE: Derived from X Protein of Hepatitis B virus
 ; FILE REFERENCE: 01336/OE154
 ; CURRENT APPLICATION NUMBER: US/09/989,621
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 09/051,006
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Hepatitis B virus
 ; US-09-989-621-2

Query Match 100.0%; Score 45; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHRTGL 9

Db 1 VLHRTGL 9

RESULT 2

US-10-209-264-5

; Sequence 5, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USES THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladas & Parry

STREET: 26 West 61 Street

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/209,264

FILING DATE: 31-Jul-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/SG98/00046

FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-209-264-5

Query Match 86.7%; Score 39; DB 15; Length 154;

Best Local Similarity 88.9%; Pred. No. 3.4;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 5

Db 92 VLYKRTLGL 100

RESULT 3

US-10-427-442-12

; Sequence 12, Application US/10427442

; Publication No. US20030177523A1

; GENERAL INFORMATION:

; APPLICANT: Falco, Carl

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Kinney, Tony

; APPLICANT: Rafalski, Antoni

; TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme

; FILE REFERENCE: BBI403 US NA

; CURRENT APPLICATION NUMBER: US/10/427,442

; CURRENT FILING DATE: 2003-05-01

; PRIOR APPLICATION NUMBER: US/09/668,262A

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/155626

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Microsoft Office 95

; SEQ ID NO 12

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Zea mays

US-10-427-442-12

Query Match 75.6%; Score 34; DB 12; Length 293;

Best Local Similarity 75.0%; Pred. No. 67;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHKRTLGL 9

Db 208 LHRTLGV 215

RESULT 4

US-10-259-165-254

; Sequence 254, Application US/10259165

; Publication No. US20030135886A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Wang, Xun

; APPLICANT: Chang, Hur-song

; APPLICANT: Briggs, Steven P.

; APPLICANT: Cooper, Bret

; APPLICANT: Glazebrook, Jane

; APPLICANT: Goff, Stephen A.

; APPLICANT: Katagiri, Fumiyaki

; APPLICANT: Kreps, Joel

; APPLICANT: Moughamer, Todd

; APPLICANT: Provart, Nicholas

; APPLICANT: Ricke, Darrell

; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

; FILE REFERENCE: 70030-NP

; CURRENT APPLICATION NUMBER: US/10/259,165

; PRIOR FILING DATE: 2002-09-26

; PRIOR APPLICATION NUMBER: US 60/370,620

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/368,327

; PRIOR FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: US 60/325,277

; PRIOR FILING DATE: 2001-09-26

; NUMBER OF SEQ ID NOS: 782

; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta

; SEQ ID NO 254

; LENGTH: 691

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: X region

; LOCATION: (278)..(278)

; OTHER INFORMATION: Xaa = any naturally occurring amino acid

US-10-259-165-254

Query Match

Best Local Similarity 75.6%; Score 34; DB 12; Length 691;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 8

Db 369 VLHKRVIG 376

RESULT 5

US-09-938-795A-1

; Sequence 1, Application US/09938795A

; Publication No. US20030045688A1

; GENERAL INFORMATION:

; APPLICANT: CHU, CHARLES CHIYUAN

; APPLICANT: CHAVAN, SANGEETA S.

; APPLICANT: MASON, JAMES M.

; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN

; FILE REFERENCE: LIJ-9000-US


```

; CURRENT APPLICATION NUMBER: US/09/938,795A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-938-795A-1

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Query Match 73.3%; Score 33; DB 11; Length 630;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

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```

2Y 1 VLHK--RTLGL 9
   :|||:|||||
3b 122 ILHKLRTLGL 132

```

```

RESULT 6
JS-10-156-761-10822
; Sequence 10822, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10822
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; JS-10-156-761-10822

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Query Match 71.1%; Score 32; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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2Y 1 VLHKRTLGL 9
   :||:|||||
3b 81 VMHNQTLGI 89

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RESULT 7
JS-09-815-242-10596
; Sequence 10596, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A

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; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10596
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-815-242-10596

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Query Match 71.1%; Score 32; DB 9; Length 448;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLHKRTLGL 9
   :||:|||||
DB 263 VIHEKSLGL 271

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RESULT 8
US-09-815-242-10278
; Sequence 10278, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10278
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-815-242-10278

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Query Match 71.1%; Score 32; DB 9; Length 748;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLG 7
 Db 378 VLHRTLG 384

RESULT 9

US-09-815-242-13880
 ; Sequence 5230, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13880
 ; LENGTH: 748
 ; TYPE: PRT
 ; ORGANISM: Salmonella typhi
 ; US-09-815-242-13880

Query Match 71.1%; Score 32; DB 9; Length 748;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLG 7
 Db 378 VLHRTLG 384

RESULT 10

US-09-815-242-5230
 ; Sequence 5230, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; Prokaryotes

FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5230
 ; LENGTH: 869
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-242-5230

Query Match 71.1%; Score 32; DB 9; Length 869;
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHRTLG 8
 Db 569 ILHRTVG 576

RESULT 11

US-09-815-242-12526
 ; Sequence 12526, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12526
 ; LENGTH: 882
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-242-12526

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Query Match          71.1%; Score 32; DB 9; Length 882;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 582 ILHKRVVG 589

RESULT 12
US-10-001-870-215
; Sequence 215, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heive
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-870-215

Query Match          68.9%; Score 31; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 8 VVEKRTLGL 16

RESULT 13
US-10-050-704-148
; Sequence 148, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-148

Query Match          68.9%; Score 31; DB 15; Length 65;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 LHKRTLG 8
DB 58 LHPRTL 64

RESULT 14
US-10-050-704-307
; Sequence 307, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 307
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-307

Query Match          68.9%; Score 31; DB 15; Length 72;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHKRTLG 8
DB 65 LHPRTL 71

RESULT 15
US-09-872-153-22
; Sequence 22, Application US/09872153
; Patent No. US20020082207A1
; GENERAL INFORMATION:
; APPLICANT: Hirst, Shannon K.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.531
; CURRENT APPLICATION NUMBER: US/09/872,153
; CURRENT FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-153-22

Query Match          68.9%; Score 31; DB 9; Length 320;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 146 VLHQRTLG 153

Search completed: December 23, 2003, 08:52:48
Job time : 79.4 secs
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GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
 CM protein - protein search, using sw model
 Run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
 (without alignments)
 78.683 Million cell updates/sec

Title: US-09-989-621-2
 Perfect score: 45
 Sequence: 1 VLHKRTLGL 9
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
 Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: PIR 76.*

1: PIR1.*
 2: PIR2.*
 3: PIR3.*
 4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	45	100.0	134	1 B48345	gene X protein, tr
2	45	100.0	154	1 QQVLD1	gene X protein - h
3	45	100.0	154	1 QQVLBH	gene X protein - h
4	45	100.0	154	1 A48345	gene X protein - h
5	45	100.0	154	1 QQVLA1	gene X protein - h
6	45	100.0	154	1 QQVLAW	gene X protein - h
7	45	100.0	154	1 QQVLKS	gene X protein - h
8	45	100.0	154	1 QQVLCP	gene X protein - h
9	45	100.0	154	2 S20756	gene X protein - h
10	45	100.0	154	2 S47404	gene X protein - h
11	45	100.0	154	2 S47408	gene X protein - h
12	45	100.0	154	2 JS0256	gene X protein - h
13	45	100.0	154	2 S67503	gene X protein - h
14	45	100.0	154	2 JQ2228	trans-activating p
15	45	100.0	154	2 S25650	gene X protein - h
16	45	100.0	154	2 S53130	gene X protein - h
17	45	100.0	154	2 JS0603	gene X protein - h
18	45	100.0	154	2 JS0604	gene X protein - h
19	45	100.0	154	2 S33687	gene X protein - h
20	45	100.0	154	2 S12542	gene X protein - h
21	45	100.0	154	2 S32203	gene X protein - h
22	45	100.0	154	2 S22319	gene X protein - h
23	45	100.0	154	2 S20751	gene X protein - h
24	45	100.0	154	2 T13466	gene X protein - h
25	45	100.0	359	2 S04570	gene X/C fusion pr
26	42	93.3	154	2 S35529	gene X protein - h
27	42	93.3	172	2 AS8456	gene X protein - h
28	39	86.7	210	2 T13472	gene X protein - h
29	39	86.7	210	2 S12598	gene X protein - h

ALIGNMENTS

RESULT 1

B48345
 gene X protein, truncated form - hepatitis B virus
 C:Species: hepatitis B virus, HBV
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
 C:Accession: B48345
 R:Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992
 A:Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I)
 A:Reference number: A48345; MUID:92352333; PMID:1642555
 A:Accession: B48345
 A:Molecule type: DNA
 A:Residues: 1-134 <REP>
 A:Cross-references: GB:S41176; NID:G252541; PIDN:AAB22733.1; PID:G252542
 A:Note: sequence extracted from NCBI backbone (NCBIN:109914, NCBIP:109915)
 C:Genetics:
 A:Gene: X
 C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
 |||||
 Db 92 VLHKRTLGL 100

RESULT 2

QQVLD1
 gene X protein - hepatitis B virus (subtype aYW)
 C:Species: hepatitis B virus, HBV
 C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994
 C:Accession: A03719
 R:Galibert, F.; Mandart, E.; Fitoussi, P.; Tiollais, P.; Charnay, P. Nature 281, 646-650, 1979
 A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype aYW) in E. coli.
 A:Reference number: A93214; MUID:81012091; PMID:399327
 A:Accession: A03719
 A:Molecule type: DNA
 A:Residues: 1-154 <GAL>
 A:Cross-references: GB:J02203; GB:V01460
 C:Genetics:
 A:Gene: X
 C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
 |||||

pyruvate kinase-li
 pyruvate kinase-li
 n-acetylglucosamin
 probable ribosomal
 hypothetical prote
 hypothetical prote
 probable polyketid
 clipB protein VC071
 lysine decarboxyla
 ATPases with chape
 class III stressor
 SmpB protein PA476
 phosphoribosylglyc
 hypothetical prote
 erythronate-4-phos
 erythronate-4-phos

30 39 86.7 492 2 T47720
 31 39 86.7 510 2 T47704
 32 36 80.0 456 2 T40367
 33 35 77.8 147 2 A70977
 34 34 75.6 88 2 T14944
 35 34 75.6 273 2 S67622
 36 34 75.6 857 2 A82290
 37 34 75.6 2723 2 T03221
 38 33 73.3 215 2 T48554
 39 33 73.3 813 2 C97292
 40 33 73.3 813 2 G83662
 41 32 71.1 159 2 D83050
 42 32 71.1 188 2 E81437
 43 32 71.1 249 2 S76104
 44 32 71.1 378 2 D91029
 45 32 71.1 378 2 E85873

Db 92 VLHRTLGL 100

RESULT 3

QOVLBH
Gene X protein - hepatitis B virus (subtype ayw, strain PHB320)

C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, strain PHB320
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Jul-2000
C/Accession: A05237; S53144; S53173; S53195; S53210; S53217; S53222; S53224; S53235; S53280

Ribicko, V.; Pushko, P.; Dreiling, D.; Pumpen, P.; Gren, E.

FEBS Lett. 185, 208-212, 1985

A/Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.

A/Reference number: A05237; MUID:85204397; PMID:3996597

A/Accession: A05237

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-154 <BIC>

A/Cross-references: EMBL:X02496; NID:G62280; PIDN:CAB41697.1; PID:G4704317

A/Experimental source: subtype ayw, strain PHB320

Ribai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A/Reference number: S53172

A/Accession: S53144

A/Molecule type: DNA

A/Residues: 124-154 <LA1>

A/Cross-references: EMBL:X85267; NID:G736025; PIDN:CAA59548.1; PID:G736026; EMBL:X85284;

85305; EMBL:X85307; EMBL:X85308; EMBL:X85310; EMBL:X85312; EMBL:X85313; EMBL:X85315; EMBL:

A/Experimental source: isolate patient Pintus '85 et al.

A/Accession: S53173

A/Molecule type: DNA

A/Residues: 124-154 <LA2>

A/Cross-references: EMBL:X85277; NID:G736065; PIDN:CAA59575.1; PID:G736066

A/Experimental source: isolate patient Bio'90

C/Genetics:

A/Genes: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLGL 9

Db 92 VLHRTLGL 100

RESULT 4

Q48345
Gene X protein - hepatitis B virus

C/Species: hepatitis B virus, HBV

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C/Accession: A48345

A/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer

Arch. Virol. 125, 299-304, 1992

A/Reference number: A48345; MUID:92352333; PMID:1642555

A/Accession: A48345

A/Molecule type: DNA

A/Residues: 1-154 <REP>

A/Cross-references: GB:S41175; NID:G252539; PIDN:AAB27732.1; PID:G252540

A/Note: sequence extracted from NCBI backbone (NCBIN:109912, NCBI:P109913)

C/Genetics:

A/Genes: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLGL 9

Db 92 VLHRTLGL 100

RESULT 7

QOVLKS

Gene X protein - hepatitis B virus (subtype adw, strain 991)

C/Species: hepatitis B virus, HBV

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C/Accession: S10380

R.Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.

submitted to the EMBL Data Library, February 1990

Db 92 VLHRTLGL 100

RESULT 5

QOVLAI

Gene X protein - hepatitis B virus (strain alpha1)

C/Species: hepatitis B virus, HBV

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C/Accession: D34773

R.Tong, S.; Li, J.; Vitvitski, L.; Trepo, C.

Virolgy 176, 596-603, 1990

A/Title: Active hepatitis B virus replication in the presence of anti-HBe is associated

A/Reference number: A34773; MUID:90266476; PMID:2345966

A/Accession: D34773

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-154 <TON>

A/Cross-references: EMBL:M32138; NID:G329667; PIDN:AAA45504.1; PID:G329671

C/Genetics:

A/Genes: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLGL 9

Db 92 VLHRTLGL 100

RESULT 6

QOVLAW

Gene X protein - hepatitis B virus (subtype adw and adw2)

C/Species: hepatitis B virus, HBV

C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998

C/Accession: A31289; B94409; A03719

R.Lo, S.J.; Chien, M.L.; Lee, Y.H.W.

Virolgy 167, 289-292, 1988

A/Title: Characteristics of the X gene of hepatitis B virus.

A/Reference number: A31289; MUID:89045656; PMID:3188399

A/Accession: A31289

A/Molecule type: DNA

A/Residues: 1-154 <LOS>

A/Experimental source: subtype adw

R.Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.

in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad

A/Reference number: A94409

A/Accession: B94409

A/Molecule type: DNA

A/Residues: 1-154 <VAL>

A/Experimental source: subtype adw2

C/Genetics:

A/Genes: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHRTLGL 9

Db 92 VLHRTLGL 100

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A;Reference number: S10380
A;Accession: S10380
A;Molecule type: DNA
A;Residues: 1-154 <KOB>
A;Cross-references: EMBL:X51970; NID:G1155012; PIDN:CAA36231.1; PID:G60432
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 8
QQVLCF
gene X protein - hepatitis B virus (strain LSH, chimpanzee)
C;Species: hepatitis B virus, HBV
C;Date: 30-Jun-1999 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C;Accession: D28885
R;Vaadin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
A;Reference number: A92796; MUID:88258473; PMID:2838576
A;Accession: D28885
A;Molecule type: DNA
A;Residues: 1-154 <VAU>
A;Cross-references: GB:D00220; NID:G221505; PIDN:BA00160.1; PID:G221509
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 9
S20756
gene X protein - hepatitis B virus (subtype ayw, patient E)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient E
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S20756
submitted to the EMBL Data Library, March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A;Reference number: S20745
A;Accession: S20756
A;Molecule type: DNA
A;Residues: 1-154 <EAI>
A;Cross-references: EMBL:X65259; NID:G59439; PIDN:CAA46360.1; PID:G59443
A;Experimental source: subtype ayw, patient E
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 10
S47404
gene X protein - hepatitis B virus (subtype ayw4)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw4
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47404
R;Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolate
A;Reference number: S47404
A;Accession: S47404
A;Molecule type: DNA
A;Residues: 1-154 <PLU>
A;Cross-references: EMBL:Z35716; NID:G527435; PIDN:CAA84785.1; PID:G527436
A;Experimental source: subtype ayw4
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 11
S47408
gene X protein - hepatitis B virus (subtype adw2)
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47408
R;Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolate
A;Reference number: S47404
A;Accession: S47408
A;Molecule type: DNA
A;Residues: 1-154 <PLU>
A;Cross-references: EMBL:Z35717; NID:G527440; PIDN:CAA84789.1; PID:G527441
A;Experimental source: subtype adw2
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
    |||||
Db 92 VLHKRTLGL 100

RESULT 12
JS0256
gene X protein - hepatitis B virus (subtype adw, strain Japan/pJDM233)
C;Species: hepatitis B virus, HBV
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
C;Accession: JS0256
R;Okamoto, H.; Tada, F.; Sakugawa, H.; Saetsoewignjo, R.I.; Imai, M.; Miyakawa, Y.; Ma
J. Gen. Virol. 69, 2575-2583, 1988
A;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
A;Reference number: JS0253; MUID:89010694; PMID:3171552
A;Accession: JS0256
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-154 <OKA>

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A;Cross-references: GB:D00329; NID:9221497

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

RESULT 13

S67503

gene X protein - hepatitis B virus (subtype ayw3, isolate Hope CH1357)

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw3, isolate Hope CH1357

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 26-Aug-1999

C;Accession: S67503

R;Norder, H.; Ebert, J.W.; Fields, H.A.; Mushahwar, I.K.; Magnus, L.O.

Virology 218, 214-223, 1996

A;Title: Complete sequencing of a gibbon hepatitis B virus genome reveals a unique genotype

A;Reference number: S67503; PMID:96207410; PMID:8615024

A;Accession: S67503

A;Molecule type: DNA

A;Residues: 1-154 <NA>

A;Cross-references: EMBL:U46935; NID:G1814218; PIDN:AA841949.1; PID:G1814219

A;Experimental source: subtype ayw3, isolate Hope CH1357

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

RESULT 14

JQ2228

trans-activating protein X - hepatitis B virus

N;Alternate names: HBx protein

C;Species: hepatitis B virus, HBV

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 26-Aug-1999

C;Accession: JQ2228; S31794

R;Naumann, H.; Schaefer, S.; Yoshida, C.F.T.; Gaspar, A.M.C.; Repp, R.; Gerlich, W.H.

J. Gen. Virol. 74, 1627-1632, 1993

A;Title: Identification of a new hepatitis B virus (HBV) genotype from Brazil that expresses

A;Reference number: JQ2228; PMID:93346970; PMID:8345355

A;Accession: JQ2228

A;Molecule type: DNA

A;Residues: 1-154 <NA>

A;Cross-references: EMBL:X69798; NID:G59422; PIDN:CAA49453.1; PID:G59424

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

RESULT 15

S25650

gene X protein - hepatitis B virus (subtype ayw, patient D)

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw, patient D

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;Accession: S25650

R;Lai, M.Z.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.

submitted to the EMBL Data Library, September 1992

A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative

A;Reference number: S25650

A;Accession: S25650

A;Molecule type: DNA

A;Residues: 1-154 <LAI>

A;Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449

A;Experimental source: subtype ayw, patient D

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 45; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

|||||

Db 92 VLHKRTLGL 100

Search completed: December 23, 2003, 08:41:05

Job time: 12 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

run on: December 23, 2003, 08:39:57 ; Search time 6.4 Seconds
(without alignments)
66.131 Million cell updates/sec

File: US-09-989-621-2

Perfect score: 45

Sequence: 1 VLHKRTLGL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	154	1 X_HPBV2	P03166 hepatitis b
2	45	100.0	154	1 X_HPBV4	P12936 hepatitis b
3	45	100.0	154	1 X_HPBV9	P17102 hepatitis b
4	45	100.0	154	1 X_HPBVA	P24026 hepatitis b
5	45	100.0	154	1 X_HPBVI	P20975 hepatitis b
6	45	100.0	154	1 X_HPBVL	P12912 hepatitis b
7	45	100.0	154	1 X_HPBVL	P20976 hepatitis b
8	45	100.0	154	1 X_HPBVT	P20977 hepatitis b
9	45	100.0	154	1 X_HPBVT	P03499 hepatitis b
10	45	100.0	154	1 X_HPBVI	P03165 hepatitis b
11	35	77.8	144	1 RL28_DROME	Q9VZS5 drosophila
12	35	77.8	147	1 RL13_MYCTU	O06260 mycobacteri
13	34	75.6	273	1 DLH1_MOUSE	Q07505 saccharomyc
14	33	73.3	630	1 F1G1_MOUSE	Q09045 mus musculu
15	32	71.1	151	1 CV53_DICDI	Q23894 dictyosteli
16	32	71.1	159	1 SRP_PSEAE	Q8H40 pseudomonas
17	32	71.1	160	1 SRP_AZOMI	Q8K14 azotobacter
18	32	71.1	249	1 P361_SYNV3	Q55578 synechocyst
19	32	71.1	748	1 PTIP_ECOLI	P37177 escherichia
20	32	71.1	748	1 PTIP_SALTY	P37177 escherichia
21	31	68.9	121	1 RNL2_CHICK	P81476 gallus galli
22	31	68.9	268	1 Y739_MYCTU	O53802 mycobacteri
23	31	68.9	390	1 UL13_HCMVA	P16849 human cytom
24	31	68.9	461	1 GPL3_YEAST	P23263 saccharomyc
25	31	68.9	498	1 YAC3_SCHPO	Q09817 schizosacch
26	31	68.9	532	1 ERA2_CABEL	P21353 caenorhabdi
27	31	68.9	655	1 YJHG_ECOLI	P39358 escherichia
28	31	68.9	735	1 AD02_HUMAN	Q39965 homo sapien
29	31	68.9	815	1 AXH_HAEIN	P44505 haemophilus
30	31	68.9	1828	1 MV5A_RAT	Q9QY13 rattus norv
31	30	66.7	231	1 RADC_BACSU	Q02170 bacillus su
32	30	66.7	294	1 BLAC_CITDI	P22390 citrobacter
33	30	66.7	360	1 ARG1_XENLA	Q91553 xenopus lae

34 30 66.7 360 1 ARG2_XENLA
35 30 66.7 360 1 ARG3_XENLA
36 30 66.7 377 1 RPOA_CHLMU
37 30 66.7 377 1 RPOA_CHLTR
38 30 66.7 490 1 SP51_YEAST
39 30 66.7 609 1 CPAL_PSESM
40 30 66.7 856 1 CLPB_HAEIN
41 30 66.7 874 1 CLPB_BRANA
42 30 66.7 1232 1 TOP2_TRYCR
43 30 66.7 1236 1 TOP2_LEICH
44 30 66.7 1239 1 TOP2_CRIFA
45 30 66.7 1307 1 SETB_MOUSE

ALIGNMENTS

RESULT 1

X_HPBV2
ID X_HPBV2 STANDARD; PRT; 154 AA.
AC P03166; P12935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw2), and
OS Hepatitis B virus (subtype adw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CX NCBI_TaxID=10408, 106821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADW2;
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ADM;
RX MEDLINE=89045656; PubMed=3188399;
RA Lo S.J., Chien M.L., Lee Y.H.W.;
RT "Characteristics of the X gene of hepatitis B virus.";
RL Virology 167:289-292(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ADM;
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; X02763; CAA26540.1; -
DR EMBL; Z35717; CAA84789.1; -
DR EMBL; M23692; AAA56820.1; -
DR EMBL; V00866; -; NOT_ANNOTATED_CDS.
DR PIR; A31289; QOVLAW.
DR PIR; S47408; S47408.
DR InterPro; IPR000236; Transactx.
DR Pfam; PF00739; X; 1.
FT CONFLICT 80 80 E -> A (IN REF. 3).
FT CONFLICT 115 115 C -> S (IN REF. 2).
FT CONFLICT 130 131 KV -> MI (IN REF. 3).
SQ SEQUENCE 154 AA; 16583 MW; 7F2AE32A4F025670 CRC64;

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Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 2
X_HPBVA
ID X_HPBV4 STANDARD; PRT; 154 AA.
AC P12936;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyachara A., Nozaki C., Yoneyama T., Ohtono N.,
RA Matsubara K.;
RT "cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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EMBL; X01587; CAA25744.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 3
X_HPBV9
ID X_HPBV9 STANDARD; PRT; 154 AA.
AC P17102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RA Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
EMBL; X51970; CAA36231.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16553 MW; 52A0D9CEFE6DCDE0 CRC64;

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 4
X_HPBVA
ID X_HPBVA STANDARD; PRT; 154 AA.
AC P24026;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
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CC
EMBL; M32138; AAA45504.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16671 MW; 2CFEEA77FA5E271F CRC64;

Query Match      100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTGL 9
   |||||
Db 92 VLHKRTGL 100

RESULT 5
X_HPBVI
ID X_HPBVI STANDARD; PRT; 154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

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```

DE  Trans-activating protein X.
DS  Hepatitis B virus (subtype adw / strain Indonesia/pIDW420).
SC  Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
DX  NCBI_TaxID=10412;
UN  [1]
LN  SEQUENCE FROM N.A.
LN  MEDLINE=89010694; PubMed=3171552;
LN  Okamoto H., Tsuda F., Sakugawa H., Saastrosowignjo R.I., Imai M.,
LN  Miyakawa Y., Mayumi M.;
LN  "Typing hepatitis B virus by homology in nucleotide sequence:
LN  comparison of surface antigen subtypes.";
LN  J. Gen. Virol. 69:2575-2583(1988).
LN  -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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LN  -----
LN  EMBL; D00331; ; NOT_ANNOTATED_CDS.
LN  PIR; JS0604; JS0604.
LN  InterPro; IPR000236; TransactX.
LN  Pfam; PF00739; X; 1.
LN  SEQUENCE 154 AA; 16585 MW; C90C817E961BFEB9 CRC64;
LN  -----
LN  Query Match 100.0%; Score 45; DB 1; Length 154;
LN  Best Local Similarity 100.0%; Pred. No. 0.024;
LN  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LN  -----
LN  1 VLHRTGL 9
LN  |||||
LN  92 VLHRTGL 100
LN  -----
LN  RESULT 6
LN  X HPBVJ
LN  ID X HPBVJ STANDARD; PRT; 154 AA.
LN  AC P20876;
LN  DT 01-FEB-1991 (Rel. 17, Created)
LN  DT 01-FEB-1991 (Rel. 17, Last sequence update)
LN  DT 01-NOV-1995 (Rel. 32, Last annotation update)
LN  DE Trans-activating protein X.
LN  GN X.
LN  OS Hepatitis B virus (subtype adw / strain Japan/pJDM233).
LN  OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
LN  OX NCBI_TaxID=10413;
LN  UN [1]
LN  LN  SEQUENCE FROM N.A.
LN  LN  MEDLINE=89010694; PubMed=3171552;
LN  LN  Okamoto H., Tsuda F., Sakugawa H., Saastrosowignjo R.I., Imai M.,
LN  LN  Miyakawa Y., Mayumi M.;
LN  LN  "Typing hepatitis B virus by homology in nucleotide sequence:
LN  LN  comparison of surface antigen subtypes.";
LN  LN  J. Gen. Virol. 69:2575-2583(1988).
LN  LN  -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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LN  LN  -----
LN  LN  EMBL; D00329; ; NOT_ANNOTATED_CDS.
LN  LN  PIR; JS0256; JS0256.
LN  LN  InterPro; IPR000236; TransactX.
LN  LN  Pfam; PF00739; X; 1.
LN  LN  SEQUENCE 154 AA; 16585 MW; 512A5A07169D5CA CRC64;

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Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLHRTGL 9
DB 92 VLHRTGL 100
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RESULT 7
X HPBVL
ID X HPBVL STANDARD; PRT; 154 AA.
AC P2912;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
UN [1]
LN  LN  SEQUENCE FROM N.A.
LN  LN  MEDLINE=88258473; PubMed=2838576;
LN  LN  Vaudin M., Wollstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
LN  LN  Harrison T.J.;
LN  LN  "The complete nucleotide sequence of the genome of a hepatitis B
LN  LN  virus isolated from a naturally infected chimpanzee.";
LN  LN  J. Gen. Virol. 69:1383-1389(1988).
LN  LN  -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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LN  LN  -----
LN  LN  EMBL; D00220; BAA00160.1; -
LN  LN  PIR; D28885; QVLCPC.
LN  LN  InterPro; IPR000236; TransactX.
LN  LN  Pfam; PF00739; X; 1.
LN  LN  SEQUENCE 154 AA; 16759 MW; F6C9D7D30C16D743 CRC64;
LN  -----
Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-----
QY 1 VLHRTGL 9
DB 92 VLHRTGL 100
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RESULT 8
X HPBVO
ID X HPBVO STANDARD; PRT; 154 AA.
AC P20977;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
UN [1]
LN  LN  SEQUENCE FROM N.A.
LN  LN  MEDLINE=89010694; PubMed=3171552;
LN  LN  Okamoto H., Tsuda F., Sakugawa H., Saastrosowignjo R.I., Imai M.,
LN  LN  Miyakawa Y., Mayumi M.;
LN  LN  "Typing hepatitis B virus by homology in nucleotide sequence:

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X_HPBVY
ID X_HPBVY STANDARD; PRT; 154 AA.
AC P03165;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10418;
[1] _SEQUENCE FROM N.A.
RN RP MEDLINE=81012091; PubMed=399327;
RX Galibbert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
RA "Nucleotide sequence of the Hepatitis B virus genome (subtype ayw)
RT cloned in E. coli.;"
RL Nature 281:646-650(1979).
[2]
RN RP _SEQUENCE FROM N.A.
RC STRAIN=Latvia.
RX MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
analysis.;"
RL FEBS Lett. 185:208-212(1985).
[3]
RN RP _FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; V01460; -; NOT_ANNOTATED_CDS.
DR EMBL; X02496; CAB41697.1; -.
DR PIR; A03719; QQVLDB.
DR PIR; A05237; QQVLDB.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT VARIANT 46 46 P -> S (IN STRAIN LATVIA).
FT VARIANT 84 88 NAHQI -> KAQFF (IN STRAIN LATVIA).
FT VARIANT 102 102 A -> V (IN STRAIN LATVIA).
FT CONFLICT 26 26 R -> C (IN REF. 1).
SQ SEQUENCE 154 AA; 16618 MM; 29FD1CC9E09A34B5 CRC64;
Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLHKRTLGL 9
DB 92 VLHKRTLGL 100
[1]
RESULT 11
RL28 DROME
ID AC Q9V255; STANDARD; PRT; 144 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 60S ribosomal protein L28.
GN CG12740.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
RN RP _SEQUENCE FROM N.A.

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Query Match	77.8%;	Score 35;	DB 1;	Length 144;
Best Local Similarity	55.8%;	Pred. No. 2.9;		

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Best Local Similarity 85.7%; Pred. No. 3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHKRTLG 8
Db 84 LHKRTIG 90

RESULT 13
DLHH YEAST STANDARD; PRT; 273 AA.
AC Q07505;
DT 13-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative carboxymethylenebutenolide (EC 3.1.1.45) (Dienselactone
DE hydrolase) (DLH).
SE YDL086W.
SN YDL086W.
OS Saccharomycetes cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Wamburt R., Wedler H., Wedler E., Scharfe M.;
RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 4-carboxymethylenebut-2-en-4-olide + H(2)O = 4
CC -!- oxohex-2-enediol.
CC -!- SIMILARITY: BELONGS TO THE DIENELACTONE HYDROLASE FAMILY.
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CC -----
EMBL; Z74134; CAA98652.1; -
DR PIR; S67622; S67622.
DR SGD; S0002244; YDL086W.
DR InterPro; IPR002925; DLH.
DR Pfam; PF01738; DLH; 1.
KW Hypothetical protein; Hydrolase.
FT ACT_SITE 130 130 BY SIMILARITY.
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 223 223 BY SIMILARITY.
SQ SEQUENCE 273 AA; 30837 MW; 9A4A9B7577243D46 CRC64;

Query Match 75.6%; Score 34; DB 1; Length 273;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHKRTIGL 9
Db 156 IHSRTIGL 163

RESULT 14
FIG1_MOUSE STANDARD; PRT; 630 AA.
AC O09046; Q9CXK7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-4 induced protein 1 precursor (Fig-1 protein).
GN IL411 OR FIG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

STRAIN=CBA/J, and BALB/c;
RX MEDLINE=97225983; PubMed=9122225;
RA Chu C.C., Paul W.E.;
RT "Fig1, an interleukin 4-induced mouse B cell gene isolated by cDNA
RT representational difference analysis.",
RL Proc. Natl. Acad. Sci. U.S.A. 94:2507-2512(1997).
RN [2]
RP SEQUENCE OF 122-289 FROM N.A.
RX STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=99012997; PubMed=9798653;
RA Chu C.C., Paul W.E.;
RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
RT representational difference analysis.",
RL Mol. Immunol. 35:487-502(1998).
RN [3]
RP SEQUENCE OF 217-630 FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K.H., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
CC -!- COFACTOR: FAD (POTENTIAL).
CC -!- INDUCTION: By interleukin-4.
CC -!- SIMILARITY: BELONGS TO THE FLAVIN MONOXAMINE OXIDASE FAMILY.
CC -----
CC STRONG, TO SNAKE L-AMINO ACID OXIDASE.
CC -----
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CC -----
EMBL; U70429; AAB51353.1; -
DR EMBL; U70430; AAB51354.1; -
DR EMBL; U89428; AAC36534.1; -
DR EMBL; U89429; AAC36535.1; -
DR EMBL; AK014297; BAB29253.1; ALT_INIT.
DR MGD; MGI:109552; IL411.
DR InterPro; IPR000759; Adrnxd reductase.
DR InterPro; IPR001613; Amineoxid fl.
DR InterPro; IPR002937; Amino oxidase.
DR InterPro; IPR00205; NAD binding.
DR Pfam; PF01593; Amino oxidase; 1.
DR PRINTS; PR00419; ADXRD7ASE.
DR PRINTS; PR00757; AMINEOXDASEF.
KW Oxidoreductase; Flavoprotein; FAD; Signal.
FT SIGNAL 1 21
FT CHAIN 22 630 INTERLEUKIN-4 INDUCED PROTEIN 1.
FT NP_BIND 59 115 FAD (ADP PART) (POTENTIAL)
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 385 385 R -> Q (IN REF. 3).
FT CONFLICT 598 630 PSEHVQVHGEVPEWHGHHGGSGTQMHRVGDHS -> LRSM

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YRCMGKSLSGVMGDLAPRKCTEWGTTPNRKKEVSTQLLS
OPSSQOTDHLH (IN REF. 3).
A674C5D6D89A071 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 630;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Y 1 VLHK--RTLGL 9
b 122 ILHKLCTLGL 132

RESULT 15

XS3_DICDI STANDARD; PRT; 151 AA.
C Q23894;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Cysteine proteinase 3 (EC 3.4.22.-) (Cysteine proteinase II)
(Fragment).
E E
N CP3.
S Dictyostelium discoideum (Slime mold).
X Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
X NCBI_TaxID=44689;
IN IN
IN IN
SEQUENCE FROM N.A.
IP STRAIN=ATCC 24397;
IP STRAIN=ATCC 24397;
AT Presse F., Bogdanovsky-Sequeval D., Mathieu M., Felenbok B.;
RT "Structural analysis of a developmentally regulated sequence encoding
RT for a cysteine proteinase in Dictyostelium discoideum.";
RT Mol. Genet. 203:324-332(1986).
X -|- SUBCELLULAR LOCATION: Lysosomal (Potential).
X -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
X
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X or send an email to license@isb-sib.ch).
X
X EMBL; X03930; CAA27569.1; --
X HSSP; O60911; LPH0.
X MEROPS; C01.081; --
X Dictydb; DD01062; cpxC.
X InterPro; IPR000668; Peptidase_C1.
X InterPro; IPR000169; SHprot_acsite.
X Pfam; PF00112; Peptidase_C1; 1.
X ProDom; PD000158; Peptidase_C1; 1.
X PROSITE; PS00139; THIOLESTERASE_CYS; FALSE NEG.
X PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
X PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
X Hydrolase; Thiol protease; Lysosome.
X NON_TER 1
X ACT_SITE 100 100 BY SIMILARITY.
X DISULFID 97 139 BY SIMILARITY.
X NON_TER 151 151
SQ SEQUENCE 151 AA; 17115 MW; 63952EB5DIAAD0A6 CRC64;

Query Match 71.1%; Score 32; DB 1; Length 151;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 HKRTLGL 9
Db 61 HKRNGL 67

Search completed: December 23, 2003, 08:41:47
Job time : 9.4 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignment)
98,410 Million cell updates/sec

title: US-09-989-621-2
effect score: 45
sequence: 1 VLHKRTLGL 9

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 830525 seqs, 258052604 residues
total number of hits satisfying chosen parameters: 830525

inimum DB seq length: 0
aximum DB seq length: 2000000000
ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	45	100.0	60	Q8V787	Q8V787 hepatitis b
2	45	100.0	129	Q8QVU1	Q8QVU1 hepatitis b
3	45	100.0	129	Q8QVU0	Q8QVU0 hepatitis b
4	45	100.0	129	Q8QVU5	Q8QVU5 hepatitis b
5	45	100.0	129	Q8QVU1	Q8QVU1 hepatitis b
6	45	100.0	129	Q8QVU2	Q8QVU2 hepatitis b
7	45	100.0	129	Q8QVU3	Q8QVU3 hepatitis b
8	45	100.0	129	Q8QVU0	Q8QVU0 hepatitis b
9	45	100.0	129	Q8QVU4	Q8QVU4 hepatitis b
10	45	100.0	129	Q8QVU9	Q8QVU9 hepatitis b
11	45	100.0	129	Q8QVU7	Q8QVU7 hepatitis b
12	45	100.0	129	Q8QVU2	Q8QVU2 hepatitis b
13	45	100.0	129	Q8QVU6	Q8QVU6 hepatitis b
14	45	100.0	129	Q8QVU9	Q8QVU9 hepatitis b
15	45	100.0	130	Q91SG7	Q91SG7 hepatitis b
16	45	100.0	130	Q91R67	Q91R67 hepatitis b

17	45	100.0	130	12	Q9DKT3	Q9DKT3 hepatitis b
18	45	100.0	130	12	Q98WJ3	Q98WJ3 hepatitis b
19	45	100.0	130	12	Q9DKT4	Q9DKT4 hepatitis b
20	45	100.0	131	12	Q98WJ2	Q98WJ2 hepatitis b
21	45	100.0	131	12	Q9DKR1	Q9DKR1 hepatitis b
22	45	100.0	134	12	Q91SG6	Q91SG6 hepatitis b
23	45	100.0	134	12	Q9C0U3	Q9C0U3 hepatitis b
24	45	100.0	134	12	Q97977	Q97977 hepatitis b
25	45	100.0	134	12	Q9WP86	Q9WP86 hepatitis b
26	45	100.0	134	12	Q9WP53	Q9WP53 hepatitis b
27	45	100.0	134	12	Q98850	Q98850 hepatitis b
28	45	100.0	134	12	Q9DKR0	Q9DKR0 hepatitis b
29	45	100.0	134	12	Q91163	Q91163 hepatitis b
30	45	100.0	134	12	Q91114	Q91114 hepatitis b
31	45	100.0	134	12	Q9WP66	Q9WP66 hepatitis b
32	45	100.0	137	12	O12409	O12409 hepatitis b
33	45	100.0	147	12	Q91SB9	Q91SB9 hepatitis b
34	45	100.0	147	12	Q91SG8	Q91SG8 hepatitis b
35	45	100.0	151	12	Q9DKQ9	Q9DKQ9 hepatitis b
36	45	100.0	151	12	Q9W9S1	Q9W9S1 hepatitis b
37	45	100.0	153	12	Q9YKJ6	Q9YKJ6 hepatitis b
38	45	100.0	153	12	Q9YKJ1	Q9YKJ1 hepatitis b
39	45	100.0	153	12	Q9YKJ8	Q9YKJ8 hepatitis b
40	45	100.0	153	12	Q9YKJ4	Q9YKJ4 hepatitis b
41	45	100.0	154	12	O04288	O04288 hepatitis b
42	45	100.0	154	12	Q9J0V0	Q9J0V0 hepatitis b
43	45	100.0	154	12	O09507	O09507 hepatitis b
44	45	100.0	154	12	Q9OXQ5	Q9OXQ5 hepatitis b
45	45	100.0	154	12	Q9DUH3	Q9DUH3 hepatitis b

ALIGNMENTS

RESULT 1
Q8V787 PRELIMINARY; PRT; 60 AA.
ID Q8V787
AC Q8V787
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Pre-c protein (Fragment).
GN PRE-C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=256;
RA Dai E.H., Liu H.J., Song Y.J., Chen C.Y., Wang J., Yang R.F.;
RT "The relationship between mutation of the core promoter and clinical
RT types' virus replication in HBV carriers."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067464; EMB84125.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 60 AA; 6879 MW; 9657F85320F96DC1 CRC64;
Query Match Similarity 100.0%; Score 45; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLHKRTLGL 9
Db 24 VLHKRTLGL 32
RESULT 2
Q8QVU1 PRELIMINARY; PRT; 129 AA.
ID Q8QVU1
AC Q8QVU1
DT 01-JUN-2002 (T-EMBLrel. 21, Created)

JT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
OT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
SU Suzuki S., Ueda R., Miyakawa Y., Mizokami M.,
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073437; BAB91089.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13871 MW; 8809A4BE287236F8 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
Db 67 VLHKRTLGL 75

RESULT 3
Q8QVUO PRELIMINARY; PRT; 129 AA.
ID Q8QVUO
AC Q8QVUO;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
SU Suzuki S., Ueda R., Miyakawa Y., Mizokami M.,
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073438; BAB91089.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13871 MW; 8809A4BE287236F8 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
Db 67 VLHKRTLGL 75

RESULT 4
Q8QVU5 PRELIMINARY; PRT; 129 AA.
ID Q8QVU5
AC Q8QVU5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
SU Suzuki S., Ueda R., Miyakawa Y., Mizokami M.,
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073443; BAB91094.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
Db 67 VLHKRTLGL 75

RESULT 5
Q8QVT1 PRELIMINARY; PRT; 129 AA.
ID Q8QVT1
AC Q8QVT1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
SU Suzuki S., Ueda R., Miyakawa Y., Mizokami M.,
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073447; BAB91095.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 129 AA; 13825 MW; 31D2F63DF3358031 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKRTLGL 9
Db 67 VLHKRTLGL 75

RESULT 6
Q8QVU2 PRELIMINARY; PRT; 129 AA.
ID Q8QVU2
AC Q8QVU2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE X protein (Fragment).
EN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

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{ NCBI_TaxID=10407;
  [1]
  MEDLINE=21912118; PubMed=11915040;
  SEQUENCE FROM N.A.
  Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
  Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
  "Hepatitis B e antigen in sera from individuals from patients with
  hepatitis B virus of genotype G.";
  Hepatology 35:922-929(2002).
  EMBL; AB073436; BAB91087.1; -.
  InterPro; IPR000236; TransactX.
  Pfam; PF00739; X; 1.
  NON_TER 1
  SEQUENCE 129 AA; 13837 MW; 8809B55FD863D708 CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 VLHRTLGL 9
| | | | |
67 VLHRTLGL 75

RESULT 7
SQVT3 PRELIMINARY; PRT; 129 AA.
D Q8QVT3;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
MEDLINE=21912118; PubMed=11915040;
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
"Hepatitis B e antigen in sera from individuals from patients with
hepatitis B virus of genotype G.";
Hepatology 35:922-929(2002).
EMBL; AB073445; BAB91096.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON_TER 1
SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 VLHRTLGL 9
| | | | |
67 VLHRTLGL 75

RESULT 8
SQVT0 PRELIMINARY; PRT; 129 AA.
D Q8QVT0;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
MEDLINE=21912118; PubMed=11915040;
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
"Hepatitis B e antigen in sera from individuals from patients with
hepatitis B virus of genotype G.";
Hepatology 35:922-929(2002).
EMBL; AB073444; BAB91095.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON_TER 1
SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 VLHRTLGL 9
| | | | |
67 VLHRTLGL 75

RESULT 9
SQVT4 PRELIMINARY; PRT; 129 AA.
D Q8QVT4;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
MEDLINE=21912118; PubMed=11915040;
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
"Hepatitis B e antigen in sera from individuals from patients with
hepatitis B virus of genotype G.";
Hepatology 35:922-929(2002).
EMBL; AB073444; BAB91095.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON_TER 1
SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 VLHRTLGL 9
| | | | |
67 VLHRTLGL 75

RESULT 10
SQVT9 PRELIMINARY; PRT; 129 AA.
D Q8QVT9;
I 01-JUN-2002 (TReMBLrel. 21, Created)
I 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
I 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
E X protein (Fragment).
X.
S Hepatitis B virus.
S Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
MEDLINE=21912118; PubMed=11915040;
Kato H., Orito E., Gish R.G., Bzowej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
"Hepatitis B e antigen in sera from individuals from patients with
hepatitis B virus of genotype G.";
Hepatology 35:922-929(2002).
EMBL; AB073445; BAB91096.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON_TER 1
SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 VLHRTLGL 9
| | | | |
67 VLHRTLGL 75
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RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073449; BAB91100.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13855 MW; 2809A272B87346EE CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 VLHKRTLGL 9
DB 67 VLHKRTLGL 75

RESULT 11
Q8QVT7 PRELIMINARY; PRT; 129 AA.
AC Q8QVT7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073441; BAB91092.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13836 MW; 280106380875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 67 VLHKRTLGL 75

RESULT 12
Q8QVT2 PRELIMINARY; PRT; 129 AA.
AC Q8QVT2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).

DR EMBL; AB073446; BAB91097.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 67 VLHKRTLGL 75

RESULT 13
Q8QVT6 PRELIMINARY; PRT; 129 AA.
AC Q8QVT6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073442; BAB91093.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 129 AA; 13837 MW; 2809A4B42875802E CRC64;

Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 67 VLHKRTLGL 75

RESULT 14
Q8QVT9 PRELIMINARY; PRT; 129 AA.
AC Q8QVT9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
ON NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21912118; PubMed=11915040;
RA Kato H., Orito E., Gish R.G., Browej N., Newsom M., Sugauchi F.,
Suzuki S., Ueda R., Miyakawa Y., Mizokami M.;
RT "Hepatitis B e antigen in sera from individuals from patients with
RT hepatitis B virus of genotype G.";
RL Hepatology 35:922-929(2002).
DR EMBL; AB073439; BAB91090.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.

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NON TER 1
SEQUENCE 129 AA; 13855 MW; F572172732148C1F CRC64;
Query Match 100.0%; Score 45; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VLHKRTILGL 9
|||||
67 VLHKRTILGL 75

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RESULT 15

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Q1SG7 PRELIMINARY; PRT; 130 AA.
Q1SG7;
01-DEC-2001 (TremBrel. 19, Created)
01-DEC-2001 (TremBrel. 19, Last sequence update)
01-MAR-2002 (TremBrel. 20, Last annotation update)
X mutant protein.
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
[1]
SEQUENCE FROM N.A.
Dong J., Cheng J., Wang Q.;
"HEV quasispecies: X gene as an example.";
Submitted (MAR-2001) to the EMBL/GenBank/DBSJ databases.
EMBL; AF355783; AAK51832.1; -.
InterPro: IPR000236; TransactX.
Pfam: PF00739; X; 1.
SEQUENCE 130 AA; 14057 MW; 3AA3F9A206D3E31A CRC64;
Query Match 100.0%; Score 45; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VLHKRTILGL 9
|||||
92 VLHKRTILGL 100

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Search completed: December 23, 2003, 08:46:09
 Job time : 25.6 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

! protein - protein search, using sw model

in on: December 23, 2003, 08:41:18 ; Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

tle: US-09-989-621-2

fect score: 45

quence: 1 VLHKTGL 9

oring table: BLOSUM62

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otal number of hits satisfying chosen parameters: 328717

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imum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCFUS-COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/PCFUS-COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	4 US-09-051-006-2	Sequence 2, Appli
2	45	100.0	153	6 5196194-20	Patent No. 5196194
3	45	100.0	153	6 5204446-4	Patent No. 5204446
4	45	100.0	154	6 5183734-1	Patent No. 5183734
5	41	91.1	21	6 5183734-7	Patent No. 5183734
6	39	86.7	154	4 US-09-719-528A-5	Sequence 5, Appli
7	37	82.2	324	4 US-09-134-001C-4996	Sequence 4996, Ap
8	36	80.0	448	4 US-09-252-991A-31654	Sequence 31654, A
9	35	77.8	147	4 US-09-732-210-576	Sequence 576, App
10	34	75.6	828	4 US-09-252-991A-31556	Sequence 31556, A
11	32	71.1	250	4 US-09-252-991A-26943	Sequence 26943, A
12	32	71.1	515	4 US-09-252-991A-24984	Sequence 24984, A
13	32	71.1	599	3 US-09-357-251-14	Sequence 14, Appli
14	32	71.1	871	4 US-09-134-001C-3979	Sequence 3979, Ap
15	31	68.9	299	1 US-08-118-270-77	Sequence 77, Appli
16	31	68.9	299	5 PCT-US93-08288-77	Sequence 77, Appli
17	31	68.9	645	4 US-09-252-991A-22095	Sequence 22095, A
18	31	68.9	651	1 US-08-264-101-2	Sequence 2, Appli
19	31	68.9	651	2 US-08-765-243-2	Sequence 2, Appli
20	31	68.9	651	5 PCT-US95-07295-2	Sequence 2, Appli
21	31	68.9	734	2 US-08-765-243-8	Sequence 8, Appli
22	31	68.9	734	5 PCT-US95-07295-8	Sequence 8, Appli
23	31	68.9	1017	4 US-09-252-991A-17291	Sequence 17291, A
24	30.5	67.8	24	6 5183734-15	Patent No. 5183734
25	30	66.7	93	4 US-08-858-207A-521	Sequence 521, App
26	30	66.7	219	4 US-09-252-991A-29479	Sequence 29479, A
27	30	66.7	244	4 US-09-252-991A-23531	Sequence 23531, A

Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 202, App
Sequence 202, App
Sequence 22411, A
Sequence 12, Appli
Sequence 5796, Ap
Sequence 4, Appli
Sequence 26221, A
Sequence 31010, A
Sequence 24910, A
Sequence 28199, A
Sequence 23274, A
Sequence 4861, Ap
Sequence 4537, Ap
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-051-006-2

; Sequence 2, Application US/09051006

; Patent No. 6380359

; GENERAL INFORMATION:

; APPLICANT: Mogam Biotechnology Research Institute

; APPLICANT: Kim, Tae-Young

; APPLICANT: Lee, Ki-Young

; APPLICANT: Chang, Jin-Soo

; APPLICANT: Cho, Sung-Yoo

; APPLICANT: Hwang, Yu-Kyeong

; APPLICANT: Choi, Myeong

; APPLICANT: Cheong, Hong-Seok

; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens

; FILE OF INVENTION: Derived from X Protein of Hepatitis B virus

; FILE REFERENCE: 0136/0E154

; CURRENT APPLICATION NUMBER: US/09/051.006

; CURRENT FILING DATE: 1998-03-30

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-09-051-006-2

Query Match 100.0%; Score 45; DB 4; Length 9;

Best Local Similarity 100.0%; Pred.No. 2.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHKTGL 9

Db 1 VLHKTGL 9

RESULT 2

5196194-20

; Patent No. 5196194

; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.

; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN

; NUMBER OF SEQUENCES: 21

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/679,621

; FILING DATE: 7-DEC-1984

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 513,055

; FILING DATE: 12-JUL-1983

; APPLICATION NUMBER: 107,267

; FILING DATE: 21-DEC-1979

; APPLICATION NUMBER: 41,909

FILING DATE: 24-MAY-1979

SEQ ID NO:20:

LENGTH: 153

196194-20

Query Match 100.0%; Score 45; DB 6; Length 153;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9

b 92 VLHKRTLGL 100

RESULT 3

204446-4

Patent No. 5204446

APPLICANT: KIMAZAWA, TOSHIKI;OSANAI, MASATOSHI

TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY

WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/503,239

FILING DATE: 02-APR-1990

SEQ ID NO:4:

LENGTH: 153

204446-4

Query Match

Best Local Similarity 100.0%; Score 45; DB 6; Length 153;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9

b 92 VLHKRTLGL 100

RESULT 4

5183734-1

Patent No. 5183734

APPLICANT: MORIARTY, ANN M.

TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

FOR ASSAYING SV40 HEXAG

NUMBER OF SEQUENCES: 17

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,982

FILING DATE: 17-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 54,424

FILING DATE: 26-MAY-1987

APPLICATION NUMBER: 648,142

FILING DATE: 07-SEP-1984

APPLICATION NUMBER: 587,570

FILING DATE: 08-MAR-1984

SEQ ID NO:1:

LENGTH: 154

5183734-1

Query Match

Best Local Similarity 100.0%; Score 45; DB 6; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

DB 92 VLHKRTLGL 100

RESULT 5

5183734-7

Patent No. 5183734

APPLICANT: MORIARTY, ANN M.

TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

FOR ASSAYING SV40 HEXAG

NUMBER OF SEQUENCES: 17

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,982

FILING DATE: 17-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 54,424

FILING DATE: 26-MAY-1987

APPLICATION NUMBER: 648,142

FILING DATE: 07-SEP-1984

APPLICATION NUMBER: 587,570

FILING DATE: 08-MAR-1984

SEQ ID NO:7:

LENGTH: 21

5183734-7

Query Match

Best Local Similarity 91.1%; Score 41; DB 6; Length 21;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 8

DB 14 VLHKRTLGL 21

RESULT 6

US-09-719-528A-5

Sequence 5, Application US/09719528A

Patent No. 6558675

GENERAL INFORMATION:

APPLICANT: Oon, Chong Jin

Lim, Gek Keow

Zhao, Yi

Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND

USES THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladas & Parry

STREET: 26 West 61 Street

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/719,528A

FILING DATE: 30-Apr-2001

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/SG98/00046

FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-719-528A-5

Query Match

Best Local Similarity 86.7%; Score 39; DB 4; Length 154;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 VLKRTLGL 9
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 92 VLYKRTLGL 100

SULT 7
 -09-134-001C-4996
 Sequence 4996 Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4996
 LENGTH: 324
 TYPE: PRT

ORGANISM: Staphylococcus epidermidis
 -09-134-001C-4996

Query Match 82.2%; Score 37; DB 4; Length 324;
 Best Local Similarity 66.7%; Pred. No. 5;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 VLKRTLGL 9
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 1 VTHKRTLV 9

RESULT 8
 S-09-252-991A-31654
 Sequence 31654 Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 31654
 LENGTH: 448
 TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
 S-09-252-991A-31654

Query Match 80.0%; Score 36; DB 4; Length 448;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 VLKRTLGL 9
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 294 VLHQRALGL 302

RESULT 9
 S-09-732-210-576
 Sequence 576 Application US/09732210
 Patent No. 6573361
 GENERAL INFORMATION:

APPLICANT: Bunkers, Greg J.
 APPLICANT: Liang, Jihong
 APPLICANT: Mittanck, Cindy A.
 APPLICANT: Seale, Jeffrey W.
 APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(15036)B
 CURRENT APPLICATION NUMBER: US/09/732,210
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,513
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: US 60/169,340
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 1753
 SEQ ID NO 576
 LENGTH: 147
 TYPE: PRT

ORGANISM: Mycobacterium tuberculosis
 US-09-732-210-576

Query Match 77.8%; Score 35; DB 4; Length 147;
 Best Local Similarity 85.7%; Pred. No. 5.8;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKXRTLG 8
 ||:|||||
 DB 84 LKXRTIG 90

RESULT 10
 US-09-252-991A-31556
 Sequence 31556 Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 31556
 LENGTH: 828
 TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-31556

Query Match 75.6%; Score 34; DB 4; Length 828;
 Best Local Similarity 85.7%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKXRTLG 8
 ||:|||||
 DB 740 LKXRTLG 746

RESULT 11
 US-09-252-991A-26943
 Sequence 26943 Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26943
LENGTH: 250
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
IS-09-252-991A-26943

Query Match 71.1%; Score 32; DB 4; Length 250;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 180 LLHKRELG 187
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RESULT 12
US-09-252-991A-24984
Sequence 24984, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24984
LENGTH: 515
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
IS-09-252-991A-24984

Query Match 71.1%; Score 32; DB 4; Length 515;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9
DB 211 VVHRSVGL 219
:|:|:|

RESULT 13
US-09-357-251-14
Sequence 14, Application US/09357251
Patent No. 6271441
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famedo, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminocacyl-tRNA Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/093,530
PRIOR FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 599
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (392)..(393)..(394)

US-09-357-251-14

Query Match 71.1%; Score 32; DB 3; Length 599;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 132 IMHKRTSG 139
:|||||

RESULT 14
US-09-134-001C-3979
Sequence 3979, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3979
LENGTH: 871
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3979

Query Match 71.1%; Score 32; DB 4; Length 871;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHKRTLG 8
DB 571 ILHKRVVG 578
:|||||

RESULT 15
US-08-118-270-77
Sequence 77, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 299 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

-08-118-270-77

Query Match 68.9%; Score 31; DB 1; Length 299;

Best Local Similarity 100.0%; Pred.No. 81;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKKT 6

|||||

100 VLHKKT 105

Search completed: December 23, 2003, 08:53:47

Search time: 11.6 secs

GenCore version 5.1.6
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1 protein - protein search, using sw model

in on: December 23, 2003, 08:41:18 ; Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

file: US-09-989-621-3

effect score: 42

sequence: 1 AMSTTDLEA 9

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

sarched: 328717 seqs, 42310858 residues

otal number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pap.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/5A.COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/5B.COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	4	US-09-051-006-3
2	42	100.0	15	6	5183734-2
3	42	100.0	16	2	US-08-675-631-6
4	42	100.0	16	6	5183734-16
5	42	100.0	17	6	5183734-8
6	42	100.0	153	6	5196194-20
7	42	100.0	153	6	5204446-4
8	42	100.0	154	4	US-09-719-528A-5
9	42	100.0	154	6	5183734-1
10	38	90.5	9	3	US-08-159-339A-335
11	38	90.5	9	4	US-09-311-784A-210
12	33	78.6	10	3	US-08-159-339A-451
13	33	78.6	15	3	US-08-159-339A-116
14	33	78.6	143	4	US-08-858-207A-441
15	32	76.2	9	3	US-08-159-339A-338
16	32	76.2	147	4	US-09-732-210-562
17	31	73.8	469	3	US-08-985-335-5
18	31	73.8	469	3	US-09-410-372-5
19	31	73.8	1165	2	US-08-640-389A-11
20	31	73.8	1165	2	US-08-599-455B-4
21	31	73.8	1165	3	US-09-093-814-1
22	31	73.8	1165	3	US-09-069-781B-4
23	31	73.8	1165	4	US-08-618-957A-11
24	31	73.8	1165	4	US-09-137-132-4
25	31	73.8	1165	4	US-08-864-564A-4
26	31	73.8	1165	4	US-09-094-410-4
27	31	73.8	1165	4	US-08-708-123D-4

Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 422, App
Sequence 411, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 57, Appl
Sequence 5150, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 93, Appli

ALIGNMENTS

RESULT 1

US-09-051-006-3
; Sequence 3, Application US/09051006
; Patent No. 6380359
; GENERAL INFORMATION:
; APPLICANT: Mogan Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/OE154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-3

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9

Db 1 AMSTTDLEA 9

RESULT 2

5183734-2
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984

APPLICATION NUMBER: 587,570
FILING DATE: 08-MAR-1984
SEQ ID NO: 2
LENGTH: 15
183734-2

Query Match 100.0%; Score 42; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 3 AMSTTDLEA 11

RESULT 3
US-08-675-631-6
Sequence 6, Application US/08675631
Patent No. 5985829
GENERAL INFORMATION:
APPLICANT: Harris, Curtis C.
APPLICANT: Wang, Xin Wei
APPLICANT: Hosiymakers, Jan H.J.
TITLE OF INVENTION: Screening Assays for Compounds That
TITLE OF INVENTION: Cause Apoptosis and Related Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,631
FILING DATE: NO. 5985829 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/359,316
FILING DATE: 19-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-225-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-16
OTHER INFORMATION: /note= "peptide # 99 irrelevant peptide
from HBV"
US-08-675-631-6

Query Match 100.0%; Score 42; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 4 AMSTTDLEA 12

RESULT 4
5183734-16
Patent No. 5183734
APPLICANT: MORIARTY, ANN M.
TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
FOR ASSAYING SV40 HEXAG
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,982
FILING DATE: 17-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 54,424
FILING DATE: 26-MAY-1987
APPLICATION NUMBER: 648,142
FILING DATE: 07-SEP-1984
APPLICATION NUMBER: 587,570
FILING DATE: 08-MAR-1984
SEQ ID NO: 16
LENGTH: 16
5183734-16

Query Match 100.0%; Score 42; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 3 AMSTTDLEA 11

RESULT 5
5183734-8
Patent No. 5183734
APPLICANT: MORIARTY, ANN M.
TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
FOR ASSAYING SV40 HEXAG
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,982
FILING DATE: 17-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 54,424
FILING DATE: 26-MAY-1987
APPLICATION NUMBER: 648,142
FILING DATE: 07-SEP-1984
APPLICATION NUMBER: 587,570
FILING DATE: 08-MAR-1984
SEQ ID NO: 8
LENGTH: 17
5183734-8

Query Match 100.0%; Score 42; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 4 AMSTTDLEA 12

RESULT 6
5196194-20
Patent No. 5196194
APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,621
FILING DATE: 7-DEC-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 513,055

FILING DATE: 12-JUL-1983
 APPLICATION NUMBER: 107,267
 FILING DATE: 21-DEC-1979
 APPLICATION NUMBER: 41,909
 FILING DATE: 24-MAY-1979
 EQ ID NO: 20
 LENGTH: 153
 96194-20

Query Match 100.0%; Score 42; DB 6; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AMSTTDLEA 9
 |||||
 102 AMSTTDLEA 110

SULT 7
 04446-4
 Patent No. 5204446
 APPLICANT: KUNAZAWA, TOSHIKAKI, OSANAI, MASATOSHI
 TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
 WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
 NUMBER OF SEQUENCES: 4
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/503,239
 FILING DATE: 02-APR-1990
 SEQ ID NO: 4
 LENGTH: 153
 104446-4

Query Match 100.0%; Score 42; DB 6; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AMSTTDLEA 9
 |||||
 102 AMSTTDLEA 110

RESULT 8
 3-09-719-528A-5
 Sequence 5, Application US/09719528A
 Patent No. 6558675
 GENERAL INFORMATION:
 APPLICANT: Oot, Chong Jin
 Lim, Gek Keow
 Zhao, Yi
 Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
 USES THEREOF

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladas & Parry
 STREET: 26 West 61 Street
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10023

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/719,528A
 FILING DATE: 30-Apr-2001
 CLASSIFICATION DATA:

PRIOR APPLICATION NUMBER: 435
 APPLICATION NUMBER: PCT/SG98/00046
 FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.
 REGISTRATION NUMBER: 30,086
 REFERENCE/DOCKET NUMBER: U-013109-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 708-1800
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-719-528A-5

Query Match 100.0%; Score 42; DB 4; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 9
 5183734-1
 Patent No. 5183734
 APPLICANT: MORIARTY, ANN M.
 TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
 FOR ASSAYING SV40 HEXAG
 NUMBER OF SEQUENCES: 17
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,982
 FILING DATE: 17-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 54,424
 FILING DATE: 26-MAY-1987
 APPLICATION NUMBER: 648,142
 FILING DATE: 07-SEP-1984
 APPLICATION NUMBER: 587,570
 FILING DATE: 08-MAR-1984
 SEQ ID NO: 1
 LENGTH: 154
 5183734-1

Query Match 100.0%; Score 42; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 10
 US-08-159-339A-335
 Sequence 335, Application US/08159339A
 Patent No. 6037135
 GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 335:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
S-08-159-339A-335

Query Match 90.5%; Score 38; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 MSTTDLEA 9
b 1 MSTTDLEA 8

RESULT 11
IS-09-311-784A-210
Sequence 210, Application US/09311784A
Patent No. 6534482

GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro

APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01

CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751

PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 210
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
IS-09-311-784A-210

Query Match 90.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTTDLEA 9
Db 1 MSTTDLEA 8

RESULT 12
US-08-159-339A-451
Sequence 451, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.

APPLICANT: Sette, Alessandro
APPLICANT: Celis, Eteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-451

Query Match 78.8%; Score 33; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 STTDLEA 9
Db 1 STTDLEA 7

RESULT 13
US-08-159-339A-1116
Sequence 1116, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA

ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-005030US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:

INFORMATION FOR SEQ ID NO: 1116:

SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

3-08-159-339A-1116

Query Match 78.6%; Score 33; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.75;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 STTDLEA 9
 1 STTDLEA 7

RESULT 14
 3-08-858-207A-441
 Sequence 441, Application US/08858207A
 Patent No. 6348328

GENERAL INFORMATION:
 APPLICANT: Black, Michael
 APPLICANT: Hodgson, John
 APPLICANT: Knowles, David
 APPLICANT: Nicholas, Richard
 APPLICANT: Stodola, Robert
 TITLE OF INVENTION: No. 6348328a1 Compounds
 NUMBER OF SEQUENCES: 552
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA

ZIP: 19406-0939
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/858,207A
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/017670
 FILING DATE: 14-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimmi, Edward R

REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P50475
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 TELEX:

INFORMATION FOR SEQ ID NO: 441:

SEQUENCE CHARACTERISTICS:
 LENGTH: 143 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6348328e

US-08-858-207A-441

Query Match 78.6%; Score 33; DB 4; Length 143;
 Best Local Similarity 77.8%; Pred. No. 9.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AMSTTDLEA 9
 DB 93 ALSTPDLEA 101

RESULT 15

US-08-159-339A-338
 Sequence 338, Application US/08159339A
 Patent No. 6037135

GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396

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; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 338:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-338

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Query Match 76.2%; Score 32; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY / 2 MSTTDLEA 9
Db 1 MSPTDLEA 8

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Job time : 11.6 secs

GenCore version 5.1.6
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effect score: 42
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otal number of hits satisfying chosen parameters: 696363

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	42	100.0	9	10	US-09-989-621-3
2	42	100.0	154	15	US-10-209-264-5
3	38	90.5	9	12	US-10-371-069-210
4	38	90.5	9	12	US-10-371-645-210
5	38	90.5	9	12	US-10-371-260-210
6	32	76.2	525	10	US-09-881-752A-96
7	31	73.8	133	15	US-10-038-010-42
8	31	73.8	308	15	US-10-038-010-46
9	31	73.8	346	9	US-09-925-301-1211
10	31	73.8	469	9	US-09-894-657-5
11	31	73.8	1165	8	US-08-779-457-2
12	31	73.8	1165	14	US-10-079-625-4
13	31	73.8	1165	14	US-10-095-929-11
14	31	73.8	1165	15	US-10-214-802-2
15	31	73.8	1165	15	US-10-226-579-4

Sequence 2129, Ap
Sequence 8314, Ap
Sequence 7969, Ap
Sequence 16, Appl
Sequence 57, Appl
Sequence 109, Appl
Sequence 10433, A
Sequence 93, Appl
Sequence 4099, Ap
Sequence 976, App
Sequence 976, App
Sequence 4748, Ap
Sequence 5719, Ap
Sequence 32, Appl
Sequence 6917, Ap
Sequence 222, App
Sequence 8, Appl
Sequence 2, Appl
Sequence 4959, Ap
Sequence 217, App
Sequence 6332, Ap
Sequence 2, Appl
Sequence 7043, Ap
Sequence 19, Appl
Sequence 7010, Ap
Sequence 947, App
Sequence 12, Appl
Sequence 4, Appl
Sequence 10933, A

16 71.4 109 12 US-10-094-749-2129
17 69.0 208 15 US-10-156-761-8314
18 69.0 212 15 US-10-156-761-7969
19 64.0 212 15 US-10-047-676A-16
20 69.0 945 14 US-10-262-794A-57
21 69.0 945 15 US-10-242-056-57
22 69.0 1726 12 US-10-205-219-109
23 69.0 4695 15 US-10-156-761-10433
24 66.7 69 15 US-10-062-548-93
25 66.7 75 11 US-09-764-891-4099
26 66.7 114 9 US-09-925-299-976
27 66.7 114 11 US-09-925-299-976
28 66.7 222 10 US-09-738-626-4748
29 66.7 287 10 US-09-738-626-5719
30 66.7 310 15 US-10-146-772-32
31 66.7 317 10 US-09-738-626-6917
32 66.7 321 12 US-10-032-201B-222
33 66.7 322 10 US-09-990-415A-8
34 66.7 322 15 US-10-014-338-2
35 66.7 326 10 US-09-738-626-4959
36 66.7 335 12 US-10-032-201B-217
37 66.7 338 10 US-09-738-626-6332
38 66.7 355 10 US-09-951-769-2
39 66.7 532 12 US-10-032-585-7043
40 66.7 755 9 US-09-881-852-19
41 66.7 1274 12 US-10-032-585-7010
42 66.7 1591 12 US-10-238-075-947
43 64.3 90 10 US-09-976-059-12
44 64.3 159 12 US-10-353-174-4
45 64.3 160 15 US-10-156-761-10933

ALIGNMENTS

RESULT 1

US-09-989-621-3
; Sequence 3, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-989-621-3

Query Match 100.0%; Score 42; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMSTTDLEA 9

DB 1 AMSTTDLEA 9

RESULT 2

US-10-209-264-5
 ; Sequence 5, Application US/10209264
 ; Publication No. US20030003111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oon, Chong Jin
 ; Lim, Gek Keow
 ; Zhao, Yi
 ; Chen, Wei Ning
 ; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
 ; USES THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ladas & Parry
 ; STREET: 26 West 61 Street
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10023
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/209,264
 ; FILING DATE: 31-Jul-2002
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/SG98/00046
 ; FILING DATE: 19-JAN-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mass, Clifford J.
 ; REGISTRATION NUMBER: 30,086
 ; REFERENCE/DOCKET NUMBER: U-013109-7
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 708-1800
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 154 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-10-209-264-5
 Query Match 100.0%; Score 42; DB 15; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.37; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 3
 US-10-371-069-210
 ; Sequence 210, Application US/10371069
 ; Publication No. US20030216342A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE REFERENCE: 39963-20022.10
 ; CURRENT APPLICATION NUMBER: US/10/371,069
 ; FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: US/10/371,069
 ; SEQUENCE DESCRIPTION: US/10/371,069

US-10-371-645-210
 ; Sequence 210, Application US/10371645
 ; Publication No. US20030216343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE REFERENCE: 39963-20022.11
 ; CURRENT APPLICATION NUMBER: US/10/371,645
 ; FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 09/078,904
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 210
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
 US-10-371-645-210
 Query Match 90.5%; Score 38; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 Db 1 MSTTDLEA 8
 RESULT 4
 US-10-371-260-210
 ; Sequence 210, Application US/10371260
 ; Publication No. US20030220285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.11
 ; CURRENT APPLICATION NUMBER: US/10/371,260
 ; FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 09/078,904
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 210
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
 US-10-371-260-210
 Query Match 90.5%; Score 38; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 Db 1 MSTTDLEA 8
 RESULT 5
 US-10-371-069-210
 ; Sequence 210, Application US/10371069
 ; Publication No. US20030216342A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE Inc.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.

```

; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV adr 1521 (peptide 2.0126)
; S-10-371-260-210

Query Match          90.5%; Score 38; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 MSTTDLEA 9
  |||||
b 1 MSTTDLEA 8

RESULT 6
S-09-881-752A-96
Sequence 96, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; S-09-881-752A-96

Query Match          76.2%; Score 32; DB 10; Length 525;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
  |||||
b 208 AMKWTDDLEA 216

RESULT 7
S-10-038-010-42
Sequence 42, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain

```

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; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 42
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: hOB-receptor long form
; LOCATION: (1)..(133)
; OTHER INFORMATION:
; US-10-038-010-42

Query Match          73.8%; Score 31; DB 15; Length 133;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 2 MSTTDLE 8
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Db 86 LSTTDLE 92

RESULT 8
US-10-038-010-46
Sequence 46, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: hOB-receptor long form
; LOCATION: (1)..(308)
; OTHER INFORMATION:
; US-10-038-010-46

Query Match          73.8%; Score 31; DB 15; Length 308;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 2 MSTTDLE 8
  |||||
Db 86 LSTTDLE 92

RESULT 9
US-09-925-301-1211
Sequence 1211, Application US/09925301
Patent No. US2002052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05982
; PRIOR FILING DATE: 2000-03-08

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; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 1211
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-301-1211

Query Match 73.8%; Score 31; DB 9; Length 346;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTTDL 8
 Db 108 MSTTDL 114

RESULT 10
 US-09-694-657-5
 ; Sequence 5, Application US/09894657
 ; Patent No. US20020098569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; Inve, Henry
 ; Lal, Preeti
 ; Shah, Purvi
 ; Corley, Neil C.

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 PROLIFERATION

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/894,657

FILING DATE: 28-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/410,372

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0421 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 469 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: OVARUT01

CLONE: 815087

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-994-657-5

Query Match 73.8%; Score 31; DB 9; Length 469;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTTDL 8
 Db 231 MSTTDL 237

RESULT 11

US-08-779-457-2

; Sequence 2, Application US/08779457

; Publication No. US20020193571A1

; GENERAL INFORMATION:

; APPLICANT: Carter, Paul J.

; APPLICANT: Chiang, Nancy Y.

; APPLICANT: Kyung, Jin Kim

; APPLICANT: Matthews, William

; APPLICANT: Rodrigues, Maria L.

; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,457

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/667197

; FILING DATE: 06/20/96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/585005

; FILING DATE: 01/08/96

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0986P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1165 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-779-457-2

Query Match 73.8%; Score 31; DB 8; Length 1165;
 Best Local Similarity 85.7%; Pred. No. 6.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTTDL 8
 Db 943 LSTTDL 949

RESULT 12

US-10-079-625-4

; Sequence 4, Application US/10079625

; Publication No. US20020182676A1

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Cupepper, Janice A.

; APPLICANT: White, David W.

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US

ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/079,625

FILING DATE: 2002-FEB-19

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/019002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

S-10-079-625-4

Query Match 73.8%; Score 31; DB 14; Length 1165;

Best Local Similarity 85.7%; Pred. No. 6.8e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 2 MSTDLE 8

b 943 LSTTDL 949

RESULT 13

S-10-095-929-11

Sequence 11, Application US/10095929

Publication No. US20020197232A1

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. Ralph

Cioffi, Joseph

Zupancic, Thomas Joel

Shafer, Alan Wayne

TITLE OF INVENTION: METHODS FOR USING THE OBSE

GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
 DEVELOPMENT

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of The Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/095,929

FILING DATE: 12-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/618,957

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 008907-0033-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-095-929-11

Query Match 73.8%; Score 31; DB 14; Length 1165;

Best Local Similarity 85.7%; Pred. No. 6.8e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTDLE 8

Db 943 LSTTDL 949

RESULT 14

US-10-214-802-2

Sequence 2, Application US/10214802

Publication No. US20030004109A1

GENERAL INFORMATION:

APPLICANT: Matthews, William

Bennett, Brian

TITLE OF INVENTION: WSX RECEPTOR

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/214,802

FILING DATE: 06-Aug-2002

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-97
; APPLICATION NUMBER: 60/
; FILING DATE: 08-Jan-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P098631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1394
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-214-802-2

```

```

Query Match      73.8%; Score 31; DB 15; Length 1165;
Best Local Similarity 85.7%; Pred. NO. 6.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 MSTDLE 8
DB      943 LSTDLE 949

```

```

RESULT 15
US-10-226-579-4
; Sequence 4, Application US/10226579
; Publication NO. US20030073634A1
; GENERAL INFORMATION:
; APPLICANT: Myers, Martin
; TITLE OF INVENTION: METHODS OF TREATING OBESITY
; FILE REFERENCE: 10276-071001
; CURRENT APPLICATION NUMBER: US/10/226,579
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/314,976
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-579-4

```

```

Query Match      73.8%; Score 31; DB 15; Length 1165;
Best Local Similarity 85.7%; Pred. NO. 6.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 MSTDLE 8
DB      943 LSTDLE 949

```

```

Search completed: December 23, 2003, 08:52:49
Job time : 80.4 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

*M protein - protein search, using sw model

run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

itle: US-09-989-621-3
effect score: 42
equence: 1 AMSTTDLEA 9

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 283308 seqs, 96168682 residues

total number of hits satisfying chosen parameters: 283308

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR 76:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	42	100.0	134	1 B48345	Gene X protein, tr
2	42	100.0	154	1 QQVLD1	Gene X protein - h
3	42	100.0	154	1 A48345	Gene X protein - h
4	42	100.0	154	1 QQVLA	Gene X protein - h
5	42	100.0	154	1 QQVLA	Gene X protein - h
6	42	100.0	154	2 S20756	Gene X protein - h
7	42	100.0	154	2 S20756	Gene X protein - h
8	42	100.0	154	2 S20756	Gene X protein - h
9	42	100.0	154	2 S20756	Gene X protein - h
10	42	100.0	154	2 S20756	Gene X protein - h
11	42	100.0	154	2 S20756	Gene X protein - h
12	42	100.0	154	2 S20756	Gene X protein - h
13	42	100.0	154	2 S20756	Gene X protein - h
14	42	100.0	154	2 S20756	Gene X protein - h
15	42	100.0	154	2 S20756	Gene X protein - h
16	42	100.0	154	2 S20756	Gene X protein - h
17	42	100.0	154	2 S20756	Gene X protein - h
18	42	100.0	154	2 S20756	Gene X protein - h
19	42	100.0	154	2 S20756	Gene X protein - h
20	42	100.0	172	2 A58456	Gene X protein - h
21	42	100.0	210	2 T13472	X protein - human
22	42	100.0	210	2 T13472	Gene X protein - h
23	38	90.5	154	1 QQVLA	Gene X protein - h
24	38	90.5	154	1 QQVLA	Gene X protein - h
25	38	90.5	154	2 S47404	Gene X protein - h
26	38	90.5	359	2 S04570	Gene X protein - h
27	35	83.3	203	2 S50728	Gene X/C fusion pr
28	35	83.3	506	2 A60693	probable membrane
29	33	78.6	126	2 B95111	aerotoxis receptor lactoyglutathione

30 78.6 131 2 AB1525 hypothetical prote
31 78.6 143 2 H97979 lactoyglutathione
32 78.6 191 2 S29008 ADP-ribosylation f
33 78.6 526 2 D71805 protein-export mem
34 76.2 56 2 AB2565 hypothetical prote
35 76.2 147 2 S66576 ribosomal protein
36 76.2 154 2 E87029 hypothetical prote
37 76.2 164 2 S20525 hypothetical prote
38 76.2 503 1 F64713 protein-export mem
39 76.2 506 2 E65095 aerotoxis receptor
40 76.2 506 2 A85968 aerotoxis sensor r
41 76.2 506 2 B91123 aerotoxis sensor r
42 73.8 402 2 S47329 OXal protein precu
43 73.8 458 2 JC5193 nuclear protein H7
44 73.8 465 2 S40701 hypothetical prote
45 73.8 506 2 B84339 hypothetical prote

ALIGNMENTS

RESULT 1

B48345
Gene X protein, truncated form - hepatitis B virus
C;Species: hepatitis B virus, HBV
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C;Accession: B48345
R;Repp: R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992
A;Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I
A;Reference number: A48345; MUID:92352333; PMID:1642555
A;Accession: B48345
A;Molecule type: DNA
A;Residues: 1-134 <REP>
A;Cross-references: GB:S41176; NID:G252541; PIDN:AB22733.1; PID:G252542
A;Note: sequence extracted from NCBI backbone (NCBIN:109914, NCBI:109915)
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. NO. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||

DB 102 AMSTTDLEA 110
|||||

RESULT 2

QQVLD1
Gene X protein - hepatitis B virus (subtype ayw)

C;Species: hepatitis B virus, HBV

C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994

C;Accession: A03719

R;Calibert, F.; Mandart, E.; Fitoussi, P.; Tiollais, P.; Charnay, P.

Nature 281, 646-650, 1979

A;Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A;Reference number: A93214; MUID:81012091; PMID:399327

A;Accession: A03719

A;Molecule type: DNA

A;Residues: 1-154 <GAL>

A;Cross-references: GB:J02203; GB:V01460

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. NO. 0.075;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||

```
Db      102 AMSTTDLEA 110

RESULT 3
A49345
Gene X protein - hepatitis B virus
C/Species: hepatitis B virus, HBV
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C/Accession: A48345
R/Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,
Arch. Virol. 125, 299-304, 1992
A/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I
A/Reference number: A48345; MUID:92352333; PMID:1642555
A/Accession: A48345
A/Molecule type: DNA
A/Residues: 1-154 <REP>
A/Cross-references: GB:S41175; NID:G252539; PIDN:AB22732.1; PID:G252540
A/Note: sequence extracted from NCBI backbone (NCBIN:109912, NCSIP:109913)
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||
Db      102 AMSTTDLEA 110

RESULT 4
QQVLAW
Gene X protein - hepatitis B virus (subtype adw and adw2)
C/Species: hepatitis B virus, HBV
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C/Accession: A31289; B94409; A03719
R/Lio, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A/Title: Characteristics of the X gene of hepatitis B virus.
A/Reference number: A31289; MUID:89045656; PMID:3188399
A/Accession: A31289
A/Molecule type: DNA
A/Residues: 1-154 <LOS>
A/Experimental source: subtype adw
R/Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad
A/Reference number: A94409
A/Accession: B94409
A/Molecule type: DNA
A/Residues: 1-154 <VAL>
A/Experimental source: subtype adw2
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||
Db      102 AMSTTDLEA 110

RESULT 5
QQVLKS
Gene X protein - hepatitis B virus (subtype adw, strain 991)
C/Species: hepatitis B virus, HBV
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C/Accession: A10380
R/Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.
submitted to the EMBL Data Library, February 1990

A/Reference number: S10380
A/Accession: S10380
A/Molecule type: DNA
A/Residues: 1-154 <KOE>
A/Cross-references: EMBL:X51970; NID:G1155012; PIDN:CAA36231.1; PID:G60432
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||
Db      102 AMSTTDLEA 110

RESULT 6
S20756
Gene X protein - hepatitis B virus (subtype ayw, patient E)
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, patient E
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C/Accession: S20756
R/Lai, M.B.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A/Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati-
A/Reference number: S20745
A/Accession: S20756
A/Molecule type: DNA
A/Residues: 1-154 <LAI>
A/Cross-references: EMBL:X65259; NID:G59439; PIDN:CAA46360.1; PID:G59443
A/Experimental source: subtype ayw, patient E
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||
Db      102 AMSTTDLEA 110

RESULT 7
S47408
Gene X protein - hepatitis B virus (subtype adw2)
C/Species: hepatitis B virus, HBV
A/Variety: subtype adw2
C/Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C/Accession: S47408
R/Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A/Description: Molecular cloning and sequencing of two complete genomes of polish isolat-
A/Reference number: S47404
A/Accession: S47408
A/Molecule type: DNA
A/Residues: 1-154 <PLU>
A/Cross-references: EMBL:Z35717; NID:G527440; PIDN:CAA84789.1; PID:G527441
A/Experimental source: subtype adw2
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
      |||||
```

```
b 102 AMSTTDLEA 110

RESULT 8
S0256
ene X protein - hepatitis B virus (subtype adw, strain Japan/PJDW233)
;Species: hepatitis B virus, HBV
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
;Accession: J50256
;Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.;
; Gen. Virol. 69, 2575-2583, 1988
;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
;Reference number: J50253; MUID:89010694; PMID:3171552
;Accession: J50256
;Status: translation not shown
;Molecule type: DNA
;Residues: 1-154 <OKA>
;Cross-references: GB:D00329; NID:g221497
;Genetics:
;Gene: X
;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
|||||
b 102 AMSTTDLEA 110

RESULT 9
25650
ene X protein - hepatitis B virus (subtype ayw, patient D)
;Species: hepatitis B virus, HBV
;Variety: subtype ayw, patient D
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
;Accession: S25650
;Lai, M.E.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.
;Submitted to the EMBL Data Library, September 1992
;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati
;Reference number: S25650
;Accession: S25650
;Molecule type: DNA
;Residues: 1-154 <LAI>
;Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449
;Experimental source: subtype ayw, patient D
;Genetics:
;Gene: X
;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f 1 AMSTTDLEA 9
|||||
c 102 AMSTTDLEA 110

RESULT 10
53130
ene X protein - hepatitis B virus
;Species: hepatitis B virus, HBV
;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
;Accession: S53130
;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
;Submitted to the EMBL Data Library, March 1995
;Reference number: S53130
;Accession: S53130
;Molecule type: DNA
;Residues: 1-154 <LAI>
;Cross-references: EMBL:X85254; NID:g736003; PIDN:CAA59513.1; PID:g736007

C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||
Db 102 AMSTTDLEA 110

RESULT 11
JS0603
gene X protein - hepatitis B virus (subtype adw, strain Okinawa/pODW282)
;Species: hepatitis B virus, HBV
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
;Accession: JS0603
;Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; Me
; J. Gen. Virol. 69, 2575-2583, 1988
;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
;Reference number: JS0253; MUID:89010694; PMID:3171552
;Accession: JS0603
;Status: translation not shown
;Molecule type: DNA
;Residues: 1-154 <OKA>
;Cross-references: GB:D00330; NID:g221498
;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||
Db 102 AMSTTDLEA 110

RESULT 12
JS0604
gene X protein - hepatitis B virus (subtype adw, strain Indonesia/pIDW420)
;Species: hepatitis B virus, HBV
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
;Accession: JS0604
;Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; Me
; J. Gen. Virol. 69, 2575-2583, 1988
;Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
;Reference number: JS0253; MUID:89010694; PMID:3171552
;Accession: JS0604
;Status: translation not shown
;Molecule type: DNA
;Residues: 1-154 <OKA>
;Cross-references: GB:D00331; NID:g221499
;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
|||||
Db 102 AMSTTDLEA 110

RESULT 13
S35529
gene X protein - hepatitis B virus (subtype adr)
;Species: hepatitis B virus, HBV
```


A:Variety: subtype adr
 C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
 C:Accession: S35529
 R:Mukaido, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hikiji, K.
 Nucleic Acids Res. 20, 6105, 1992
 A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SPADR) and
 A:Reference number: S35527; MUID:93096607; PMID:1461746
 A:Accession: S35529
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-154 <UNK>
 A:Cross-references: EMBL:D12980; NID:G221500; PIDN:BAA02356.1; PID:G221503
 A:Experimental source: subtype adr
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 C:Genetics:
 A:Gene: X
 C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

RESULT 14
 S33687
 gene X protein - hepatitis B virus (subtype adw2, patient A938)
 C:Species: hepatitis B virus, HBV
 A:Variety: subtype adw2, patient A938
 C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
 C:Accession: S33687
 R:Preisler-Adams, S.; Schlager, H.J.; Peters, T.; Korp, R.; Rasenack, J.
 Nucleic Acids Res. 21, 2258, 1993
 A:Title: Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identifi
 A:Reference number: S33686; MUID:93275766; PMID:8502574
 A:Accession: S33687
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-154 <PRE>
 A:Cross-references: EMBL:X70185
 A:Experimental source: subtype adw2, patient A938
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C:Genetics:
 A:Gene: X
 C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

RESULT 15
 S12542
 gene X protein - hepatitis B virus
 C:Species: hepatitis B virus, HBV
 C:Date: 21-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 16-Feb-1997
 C:Accession: S12542
 R:Unger, T.; Shaul, Y.
 VMB J. 9, 1889-1895, 1990
 A:Title: The X protein of the hepatitis B virus acts as a transcription factor when targ
 A:Reference number: S12542; MUID:90269224; PMID:2347309
 A:Accession: S12542
 A:Molecule type: DNA
 A:Residues: 1-154 <UNG>
 C:Genetics:
 A:Gene: X

C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 42; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 Db 102 AMSTTDLEA 110

Search completed: December 23, 2003, 08:41:07
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 seconds
(without alignments)
66.131 Million cell updates/sec

Title: US-09-989-621-3
Perfect score: 42
Sequence: 1 AMSTTDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	154	1 X HPBV2	P03166 hepatitis b
2	42	100.0	154	1 X HPBV4	P12936 hepatitis b
3	42	100.0	154	1 X HPBV9	P17102 hepatitis b
4	42	100.0	154	1 X HPBV1	P20975 hepatitis b
5	42	100.0	154	1 X HPBVJ	P20976 hepatitis b
6	42	100.0	154	1 X HPBVC	P20977 hepatitis b
7	42	100.0	154	1 X HPBVY	P03165 hepatitis b
8	38	90.5	154	1 X HPBVA	P24026 hepatitis b
9	35	83.3	203	1 YNU3 YEAST	P40163 saccharomyc
10	33	78.6	190	1 ARF GIALA	P28991 giardia lam
11	33	78.6	526	1 SECD_HELPJ	P92366 helicobacte
12	32	76.2	147	1 RLAI_THETH	P36238 thermus the
13	32	76.2	503	1 SECD_HELPY	O26074 helicobacte
14	32	76.2	506	1 AER_ECOLI	P50466 escherichia
15	31	73.8	402	1 OXAI YEAST	P39952 saccharomyc
16	31	73.8	465	1 YK77 CAEEL	P34318 caenorhabdi
17	31	73.8	1163	1 LEPR_HUMAN	P94357 macaca mula
18	31	73.8	1165	1 LEPR_HUMAN	P48357 homo sapien
19	30	71.4	479	1 RP54_XANCV	P77998 xanthomonas
20	30	71.4	508	1 Y202 HUMAN	P32417 oryctolagus
21	30	71.4	530	1 FM03 RABIT	Q92599 homo sapien
22	30	71.4	644	1 VP74 NPVOP	O10365 orgyia pseu
23	30	71.4	794	1 YG2A YEAST	P53243 saccharomyc
24	30	71.4	1210	1 RPB2_SCHPO	Q02061 schizosacch
25	30	71.4	1319	1 MN1_HUMAN	Q10571 homo sapien
26	30	71.4	1690	1 RPOC_THENA	P36252 thermotoga
27	29	69.0	154	1 X HPBVL	P12912 hepatitis b
28	29	69.0	203	1 ATP4 ARATH	Q96252 arabidopsis
29	29	69.0	229	1 ARTM_ARTSA	P17720 artemia sal
30	29	69.0	241	1 SPIR_SPIVE	P21625 spiroplasma
31	29	69.0	305	1 MIAA_LISIN	Q94C59 listeria in
32	29	69.0	320	1 DIMI_KULLA	P78697 kluyveromyc
33	29	69.0	323	1 RAD1_SCHPO	P22193 schizosacch

34 29 69.0 337 1 YKP1_YEAST P36059 saccharomyc
35 29 69.0 399 1 OPS2_PATYE O15974 patinopecte
36 29 69.0 406 1 TRPB_CAUCR P12290 caulobacter
37 29 69.0 433 1 DHOM_SYNY3 P52986 synechocyst
38 29 69.0 437 1 VPS4_YEAST P52917 saccharomyc
39 29 69.0 471 1 ATPB_HERAU P42466 herpetosiph
40 29 69.0 495 1 CRTD_RHOSH Q1671 rhodobacter
41 29 69.0 743 1 CUL2_CABEL Q1790 caenorhabdi
42 29 69.0 922 1 YKP0_YEAST Q1790 caenorhabdi
43 29 69.0 1267 1 DHR1_YEAST Q4217 saccharomyc
44 28 66.7 109 1 RL37_TETTH P24002 tetrahymena
45 28 66.7 129 1 YQ09_HALN1 P58015 halobacteri

ALIGNMENTS

RESULT 1
X HPBV2
ID X HPBV2 STANDARD; PRT; 154 AA.
AC P03166; P12935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw2), and
OC Hepatitis B virus (subtype adw).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408; 106821;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=ADW2;
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=ADW;
RX MEDLINE=89045656; PubMed=3188399;
RA Lo S.J., Chien M.L., Lee Y.H.W.;
RT "Characteristics of the X gene of hepatitis B virus";
RL Virology 167:1289-292 (1988).
RN [3]
RC SEQUENCE FROM N.A.
RA STRAIN=ADW;
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757 (1983).
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CC -----
CC EMBL; X02763; CAA86540.1; -;
CC EMBL; Z35717; CAA84789.1; -;
CC EMBL; M23692; AAA56820.1; -;
CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
CC PIR; A31289; QQVLAW.
CC PIR; S47408; S47408.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC CONFLICT 80 80 E -> A (IN REF. 3).
CC CONFLICT 115 115 C -> S (IN REF. 2).
CC CONFLICT 130 131 KV -> MI (IN REF. 3).
CC SEQUENCE 154 AA; 16583 MW; 7F2AE32A4F025670 CRC64;

```

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
DB      102 AMSTTDLEA 110

RESULT 2
X HPBV4
ID X HPBV4      STANDARD;      PRT;      154 AA.
AC P12936;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyanochara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
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CC
CC EMBL; X01587; CAA25744.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
DB      102 AMSTTDLEA 110

RESULT 3
X HPBV9
ID X HPBV9      STANDARD;      PRT;      154 AA.
AC P17102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koehnel H.G., Schueler A., Lottmann S., Thomassen R.;
RA Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; X51970; CAA36231.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16553 MW; 52A0D9CEFE6DCDE0 CRC64;

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
DB      102 AMSTTDLEA 110

RESULT 4
X HPBVI
ID X HPBVI      STANDARD;      PRT;      154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Indonesia/pIDW420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tauda F., Sakugawa H., Sastrosewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC
CC EMBL; D00331; -; NOT_ANNOTATED_CDS.
CC PIR; J03604; J03604.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16556 MW; C80C817B961BFFB9 CRC64;

Query Match      100.0%; Score 42; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AMSTTDLEA 9
DB      102 AMSTTDLEA 110

RESULT 5
X HPBVJ
ID X HPBVJ      STANDARD;      PRT;      154 AA.
AC P20976;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

```

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Japan/pJDW233).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RA "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC -----
 DR EMBL; D00329; -; NOT ANNOTATED_CDS.
 DR PIR; JS0256; JS0256.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16585 MW; 512A5A077169DSCA CRC64;
 Query Match 100.0%; Score 42; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 6
 X HPBVO STANDARD; PRT; 154 AA.
 ID X HPBVO
 AC P20977;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RA "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
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 CC -----
 DR EMBL; D00330; -; NOT ANNOTATED_CDS.
 DR PIR; JS0603; JS0603.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.

SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;
 Query Match 100.0%; Score 42; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 7
 X HPBVO STANDARD; PRT; 154 AA.
 ID X HPBVO
 AC P03165;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype ayw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10418;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8102091; PubMed=399327;
 RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
 RA "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
 RT cloned in E. coli.";
 RL Nature 281:646-650(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Latvia;
 RX MEDLINE=85204397; PubMed=3996597;
 RA Bichko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
 RA "Subtype ayw variant of hepatitis B virus. DNA primary structure
 RT analysis.";
 RL FEBS Lett. 185:208-212(1985).
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 CC -----
 DR EMBL; V01460; -; NOT ANNOTATED_CDS.
 DR EMBL; X02496; CAB41697.1; -;
 DR PIR; A03719; QOVLDI.
 DR PIR; A05237; QOVLBI.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT VARIANT 46 46 P -> S (IN STRAIN LATVIA).
 FT VARIANT 84 88 NAHQI -> KAQPF (IN STRAIN LATVIA).
 FT VARIANT 102 102 A -> V (IN STRAIN LATVIA).
 FT CONFLICT 26 26 R -> C (IN REF. 1).
 SQ SEQUENCE 154 AA; 16618 MW; 29FDCC9E09A34B5 CRC64;
 Query Match 100.0%; Score 42; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 8
 X HPBVA STANDARD; PRT; 154 AA.
 ID X HPBVA
 AC P24026;

DT 01-VAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (strain alpha).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90266476; PubMed=2345966;
 RA Tong S., Li J., Vitvitski L., Trepo C.;
 RT "Active hepatitis B virus replication in the presence of anti-HBe is
 associated with viral variants containing an inactive pre-C region.";
 RL Virology 176:596-603(1990)
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 CC EMBL; M32138; AAA45504.1;
 DR PIR; D34773; QOVLAI.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1
 SQ SEQUENCE 154 AA; 16671 MW; 2CPEEA77FA5E271F CRC64;
 Query Match 90.5%; Score 38; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 DB 103 MSTTDLEA 110
 RESULT 9
 YNU3 YEAST
 ID YNU3 YEAST STANDARD; PRT; 203 AA.
 AC P40163;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Very hypothetical 22.4 kDa protein in SPX18-SPX19 intergenic region.
 GN YNL203C OR N1358.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288c / FV1679;
 RA Jonniaux J.-L., Coster F., Fumelle B., Goffeau A.;
 RT A 21.7 kb DNA segment on the left arm of yeast chromosome XIV
 carries WH13, GCR2, SPX18, SPX19, an homologue to the heat shock gene
 SSBI and 8 new open reading frames of unknown function.;
 RL Yeast 10:1639-1645(1994).
 CC [2]
 CC SEQUENCE FROM N.A.
 RA Coe J.G., Murray L.E., Dawes I.W.;
 RL Submitted (MAY 1992) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; X78898; CAA55505.1;
 DR EMBL; Z71479; CAA96102.1;
 DR EMBL; M90351; -; NOT_ANNOTATED_CDS.
 DR PIR; S50728; S50728.
 DR SGD; S0005147; YNL203C.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 89 109 POTENTIAL.
 FT CONFLICT 160 160 S -> F (IN REF. 2).
 FT CONFLICT 178 178 Y -> H (IN REF. 2).
 FT CONFLICT 183 183 X -> T (IN REF. 2).
 FT CONFLICT 186 186 F -> L (IN REF. 2).
 SQ SEQUENCE 203 AA; 22418 MW; C22CE2651E0925BB CRC64;
 Query Match 83.3%; Score 35; DB 1; Length 203;
 Best Local Similarity 77.8%; Pred. No. 1-2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 DB 23 SMSTTDLEA 31
 RESULT 10
 ARF GIALA
 ID ARF GIALA STANDARD; PRT; 190 AA.
 AC P26991;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ADP-ribosylation factor
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
 OX NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250616; PubMed=1577802;
 RA Murtagh J.J. Jr., Mowatt M.W., Lee C.-M., Lee F.-J.S., Mishima K.,
 RA Nash T.E., Moss J., Vaughan M.;
 RT "Guanine nucleotide-binding proteins in the intestinal parasite
 Giardia lamblia. Isolation of a gene encoding an approximately 20-kDa
 ADP-ribosylation factor.";
 RL J. Biol. Chem. 267:9654-9662(1992).
 CC -1- FUNCTION: GTP-BINDING PROTEIN THAT FUNCTIONS AS AN ALLOSTERIC
 ACTIVATOR OF THE CHOLERA TOXIN CATALYTIC SUBUNIT, AN ADP-
 RIBOSYLTRANSFERASE. INVOLVED IN PROTEIN TRAFFICKING; MAY MODULATE
 VESICLE BUDDING AND UNCOATING WITHIN THE GOLGI APPARATUS.
 CC -1- SIMILARITY: BELONGS TO THE ARF FAMILY OF GTP-BINDING PROTEINS.
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 CC EMBL; M86513; -; NOT_ANNOTATED_CDS.
 DR PIR; S29008; S29008.
 DR HSP; P32889; 1RRP.
 DR InterPro; IPR006688; ARF.
 DR InterPro; IPR006689; ARF/SAR.
 DR InterPro; IPR001806; Ras transfrmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00025; arf; 1.
 DR PRINTS; PR00449; RASTENSRMNG.
 DR PRINTS; PR00328; SARIGTBP.
 DR SMART; SM00177; ARF; 1.
 DR TIGRFAMs; TIGR00031; small_GTP; 1.
 DR PROSITE; PS01019; ARF; 1.
 KW GTP-binding; Myristate; Protein transport; Golgi stack.
 FT INIT_MET 0 0 BY SIMILARITY.

FT NP_BIND 23 1 MYRISTATE (POTENTIAL).
 FT NP_BIND 66 30 GTP (BY SIMILARITY).
 FT NP_BIND 127 70 GTP (BY SIMILARITY).
 FT NP_BIND 130 130 GTP (BY SIMILARITY).
 SQ SEQUENCE 190 AA; 21634 MW; B05549FA0DA49036 CRC64;

Query Match
 Best Local Similarity 78.6%; Score 33; DB 1; Length 190;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDL 7
 DB 134 AMSTTDL 140

RESULT 11
 ID _SCD_HELPJ STANDARD; PRT; 526 AA.
 AC Q2J36;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-export membrane protein.
 GN SCD OR JHP1449.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Malls S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.,
 RT Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.
 RL Nature 397:176-180(1999).
 CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
 CC -1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
 CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SECD/SECF FAMILY. SECD FAMILY.
 CC -----
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 CC -----
 CC EMBL; A5001567; AAD07024.1; --
 CC PIR; D71805; D71805.
 CC InterPro; IPR001036; Acrlvin_res.
 CC InterPro; IPR005791; SecD.
 CC InterPro; IPR003335; SecD.
 CC Pfam; PF02355; SecD SecF.1.
 CC PRINTS; PR00702; ACRIFLAVINRP.
 CC TIGRFAMs; TIGR00916; 2A0604501.1.
 CC TIGRFAMs; TIGR01129; secD.1.
 CC Protein transport; Translocation; Transmembrane; Membrane;
 CC Complete proteome.
 FT TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 356 376 POTENTIAL.
 FT TRANSMEM 379 399 POTENTIAL.
 FT TRANSMEM 453 473 POTENTIAL.
 FT TRANSMEM 478 498 POTENTIAL.
 SQ SEQUENCE 526 AA; 56796 MW; 5B4C9E505794782A CRC64;

Query Match
 Best Local Similarity 78.6%; Score 33; DB 1; Length 526;

Best Local Similarity 77.8%; Pred. NO. 11;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMSTTDL 9
 DB 208 AMSTTDL 216

RESULT 12
 ID RL11 THETH STANDARD; PRT; 147 AA.
 AC P36238;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L11.
 GN RPLK OR RPL11.
 OS Thermus thermophilus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VKI;
 RA Ossina N., Eliseikina I., Garber M.B., Jonsson B.-H.;
 RL Submitted (SFP-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN=HB8 / ATCC 27634;
 RX MEDLINE=93077476; PubMed=1447157;
 RA Heinrich T., Schroeder W., Erdmann V.A., Hartmann R.K.;
 RT Identification of the gene encoding transcription factor NusG of
 RT Thermus thermophilus.
 RL J. Bacteriol. 174:7859-7863(1992).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; X81375; CAA57138.1; --
 CC HSRP; P29395; LWS.
 CC InterPro; IPR000911; Ribosomal L11.
 CC InterPro; IPR006519; Ribosomal L11bac.
 CC Pfam; PF00298; Ribosomal L11.1.
 CC Pfam; PF03946; Ribosomal L11.N; 1.
 CC ProDom; PD001367; Ribosomal_L11; 1.
 CC SMART; SM00849; RL11; 1.
 CC TIGRFAMs; TIGR01632; L11_bact; 1.
 CC PROSITE; PS00359; RIBOSOMAL_L11; 1.
 CC Ribosomal protein; RNA-binding.
 FT VARIANT 23 23 V -> G (IN STRAIN HB8).
 SQ SEQUENCE 147 AA; 15505 MW; 3D8ECBEBE8B5FE9 CRC64;

Query Match
 Best Local Similarity 76.2%; Score 32; DB 1; Length 147;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSMTDL 9
 DB 115 MSMTDL 122

RESULT 13
 ID _SCD_HELPJ STANDARD; PRT; 503 AA.
 AC Q26074;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-export membrane protein secD.
 GN SEC2 OR HP1550.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9521185;
 RA Tomb J.-F., White O., Karlavage A.R., Clayton R.A., Sutton G.G., B.A.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RL Nature 388:539-547(1997).
 CC -!- FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
 CC -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLLOCATION APPARATUS
 CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
 CC (BY SIMILARITY)
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SEC2/SECF FAMILY. SEC2 FAMILY.
 CC
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 CC
 CC EMBL; AF000652; AAD08588.1; --
 CC PIR; F64713; F64713.
 CC TIGR; HP1550; --
 CC InterPro; IPR001036; Acrlvin_res.
 CC InterPro; IPR005791; SecD.
 CC InterPro; IPR003335; SecD_SecF.
 CC Pfam; PF02355; SecD_SecF; 1.
 CC PRINTS; PR00702; ACRIFLAVINRP.
 CC TIGRFAMs; TIGR00916; 2A0604s01; 1.
 CC TIGRFAMs; TIGR01129; secD; 1.
 CC Protein transport; Translocation; Transmembrane; Membrane;
 KW Complete proteome.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 334 354 POTENTIAL.
 FT TRANSMEM 357 377 POTENTIAL.
 FT TRANSMEM 383 403 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 SQ SEQUENCE 503 AA; 54247 MW; 8541C291CA317086 CRC64;
 Query Match 76.2%; Score 32; DB 1; Length 503;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AMSTTDLEA 9
 Db 186 AMKMTDLEA 194
 RESULT 14
 AER_ECOLI
 ID AER_ECOLI STANDARD; PRT; 506 AA.
 AC P50466;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aerotaxis receptor.
 GN AER OR AIR OR B3072.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC [2]
 CC FUNCTION
 CC MEDLINE=97334134; PubMed=9190831;
 CC Bibikov S.I., Biran R., Rudd K.E., Parkinson J.S.;
 CC "A signal transducer for aerotaxis in Escherichia coli.";
 CC J. Bacteriol. 179:4075-4079(1997).
 CC [3]
 CC FUNCTION
 CC MEDLINE=98021405; PubMed=9380671;
 CC Rebbapragada A., Johnson M.S., Harding G.P., Zuccarelli A.J.,
 CC Fletcher H.M., Zhulin I.B., Taylor B.L.;
 CC "The Aer protein and the serine chemoreceptor Tsr independently sense
 CC intracellular energy levels and transduce oxygen, redox, and energy
 CC signals for Escherichia coli behavior.";
 CC Proc. Natl. Acad. Sci. U.S.A. 94:10541-10546(1997).
 CC -!- FUNCTION: SIGNAL TRANSDUCER FOR AEROTAXIS. THE AEROTACTIC
 CC RESPONSES IS THE ACCUMULATION OF CELLS AROUND AIR BUBBLES. THE
 CC NATURE OF THE SENSORY STIMULUS DETECTED BY THIS PROTEIN IS THE
 CC PROTON MOTIVE FORCE OR CELLULAR REDOX STATE. IT USES A PAD
 CC PROSTHETIC GROUP AS A REDOX SENSOR TO MONITOR OXYGEN LEVELS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC (POTENTIAL).
 CC -!- SIMILARITY: IN THE N-TERMINAL TO NIFL AND FIXL AND OTHER PROTEINS
 CC IMPLICATED IN OXYGEN-SENSING.
 CC -!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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 CC
 CC EMBL; U28379; AA89151.1; --
 CC EMBL; A5000389; AAC76107.1; --
 CC PIR; E65095; E65095.
 CC HSP; P02942; 1Q07.
 CC EcoGene; EGI2955; aer.
 CC InterPro; IPR004089; Chmtaxis_transd.
 CC InterPro; IPR003660; HAMF.
 CC InterPro; IPR004090; Me_chemotaxis.
 CC InterPro; IPR001610; PAC.
 CC Pfam; PF00672; HAMF; 1.
 CC Pfam; PF00015; MCPsignal; 1.
 CC Pfam; PF00785; PAC; 1.
 CC PRINTS; PR00260; CHEMTRNSDUCR.
 CC SMART; SM00283; WA; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAC; 1.
 CC TIGRFAMs; TIGR00229; sensory_box; 1.
 CC PROSITE; PS50111; CHEMOTAXIS_TRANSDCU_2; 1.

KW Chemotaxis; Transducer; Transmembrane; Methylation; Periplasmic;
 KW Inner membrane; FAD; Flavoprotein; Complete proteome.
 FT DOMAIN 1 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 186 POTENTIAL.
 FT DOMAIN 187 190 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 191 209 POTENTIAL.
 FT DOMAIN 210 506 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 263 492 METHYL-ACCEPTING TRANSFERASE.
 SQ SEQUENCE 506 AA; 55065 MW; 913DEBCF14E3FD08 CRC64;
 Query Match 76.2%; Score 32; DB 1; Length 506;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 DB 21 MSTTDLQS 28
 RESULT 15
 OXAL YEAST STANDARD; PRT; 402 AA.
 AC P39952:
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome oxidase biogenesis protein OXAL, mitochondrial precursor.
 GN OXAL OR PRT1402 OR YER154W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=FL100;
 RA Bonnafoey N., Chalvet F., Hamel P., Slonimski P.P., Dujardin G.;
 RT "OXAL, a Saccharomyces cerevisiae nuclear gene whose sequence is
 RT conserved from prokaryotes to eukaryotes controls cytochrome oxidase
 RT biogenesis";
 RL J. Mol. Biol. 239:201-212(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=95115677; PubMed=7816036;
 RA Bauer M., Behrens M., Esser K., Michaelis G., Prati E.;
 RT "PRT1402, a nuclear gene required for proteolytic processing of
 RT cytochrome oxidase subunit 2 in yeast";
 RL Mol. Gen. Genet. 245:272-278(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=8288c / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
 RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA On C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V";
 RL Nature 387:78-81(1997).
 RN [4]
 RN TOPOLOGY.
 RC MEDLINE=97315163; PubMed=9171337;
 RA Herrmann J.N., Neupert W., Stuart R.A.;
 RT "Insertion into the mitochondrial inner membrane of a polytopic
 RT protein, the nuclear-encoded Oxalp.";
 RL EMBO J. 16:2217-2226(1997).
 CC -1- FUNCTION: REQUIRED FOR POST-TRANSLATIONAL STEP OF CYTOCHROME
 CC OXIDASE BIOGENESIS. SEEMS TO INVOLVE IN THE PROTEOLYTIC
 CC PROCESSING OF CYTOCHROME OXIDASE SUBUNIT 2.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE OXAL / 60 KDA IMP FAMILY.

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DR EMBL; X77558; CAA54675.1; -

DR EMBL; X74456; CAA52465.1; -

DR EMBL; U18917; AAB64681.1; -

DR PIR; S47329; S47329

DR SGD; S0000856; OXAL

DR GO; GO:0005743; C:mitochondrial inner membrane; IDA.

DR GO; GO:0008565; P:protein transporter activity; IMP.

DR GO; GO:0006628; P:mitochondrial translocation; IMP.

DR InterPro; IPR001708; 60kDa innermem.

DR Pfam; PF02096; 60KD IMP; I

DR Transmembrane; Mitochondrion; Transit peptide.

FT TRANSIT 1 42 MITOCHONDRION (POTENTIAL).

FT CHAIN 43 402 CYTOCHROME OXIDASE BIOGENESIS PROTEIN

FT DOMAIN 43 130 OXAL.

FT TRANSMEM 131 148 MITOCHONDRIAL INTERMEMBRANE (PROBABLE).

FT DOMAIN 149 200 PROBABLE.

FT TRANSMEM 201 218 MITOCHONDRIAL MATRIX (PROBABLE).

FT DOMAIN 219 246 PROBABLE.

FT TRANSMEM 247 263 MITOCHONDRIAL INTERMEMBRANE (PROBABLE).

FT DOMAIN 264 275 PROBABLE.

FT TRANSMEM 276 291 MITOCHONDRIAL MATRIX (PROBABLE).

FT DOMAIN 292 292 PROBABLE.

FT TRANSMEM 293 310 MITOCHONDRIAL INTERMEMBRANE (PROBABLE).

FT DOMAIN 311 402 MITOCHONDRIAL MATRIX (PROBABLE).

FT CONFLICT 108 108 W -> R (IN REF. 1).

SQ SEQUENCE 402 AA; 44815 MW; 10890B8F2BE67ED CRC64;

Query Match 73.8%; Score 31; DB 1; Length 402;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTTDLE 8

DB 172 MSTTDLQ 178

Search completed: December 23, 2003, 08:41:50

Job time : 9.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-3
Perfect score: 42
Sequence: 1 AMSTTDLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mnc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	42	100.0	58	12 Q9E0Q4	Q9E0Q4 hepatitis b
2	42	100.0	58	12 Q9E0P6	Q9E0P6 hepatitis b
3	42	100.0	58	12 Q9E0U2	Q9E0U2 hepatitis b
4	42	100.0	58	12 Q9E0S4	Q9E0S4 hepatitis b
5	42	100.0	58	12 Q9E0P2	Q9E0P2 hepatitis b
6	42	100.0	58	12 Q9E0S6	Q9E0S6 hepatitis b
7	42	100.0	58	12 Q9E0U0	Q9E0U0 hepatitis b
8	42	100.0	58	12 Q9E0Q2	Q9E0Q2 hepatitis b
9	42	100.0	58	12 Q9E0S2	Q9E0S2 hepatitis b
10	42	100.0	58	12 Q9E0W6	Q9E0W6 hepatitis b
11	42	100.0	58	12 Q9E0R4	Q9E0R4 hepatitis b
12	42	100.0	58	12 Q9E0P0	Q9E0P0 hepatitis b
13	42	100.0	58	12 Q9E0V2	Q9E0V2 hepatitis b
14	42	100.0	58	12 Q9E0U8	Q9E0U8 hepatitis b
15	42	100.0	58	12 Q9E0W0	Q9E0W0 hepatitis b
16	42	100.0	58	12 Q9E0U4	Q9E0U4 hepatitis b

17	42	100.0	58	12 Q9E0T0	Q9E0T0 hepatitis b
18	42	100.0	58	12 Q9E0N6	Q9E0N6 hepatitis b
19	42	100.0	58	12 Q9E0V6	Q9E0V6 hepatitis b
20	42	100.0	58	12 Q9E0P8	Q9E0P8 hepatitis b
21	42	100.0	58	12 Q9E0R0	Q9E0R0 hepatitis b
22	42	100.0	58	12 Q9E0R2	Q9E0R2 hepatitis b
23	42	100.0	58	12 Q9E0V0	Q9E0V0 hepatitis b
24	42	100.0	58	12 Q9E0T8	Q9E0T8 hepatitis b
25	42	100.0	58	12 Q9E0R6	Q9E0R6 hepatitis b
26	42	100.0	58	12 Q9E0T6	Q9E0T6 hepatitis b
27	42	100.0	58	12 Q9E0N8	Q9E0N8 hepatitis b
28	42	100.0	58	12 Q9E0U6	Q9E0U6 hepatitis b
29	42	100.0	58	12 Q9E0Q6	Q9E0Q6 hepatitis b
30	42	100.0	58	12 Q9E0N4	Q9E0N4 hepatitis b
31	42	100.0	58	12 Q9E0S0	Q9E0S0 hepatitis b
32	42	100.0	58	12 Q9E0V8	Q9E0V8 hepatitis b
33	42	100.0	60	12 Q8V787	Q8V787 hepatitis b
34	42	100.0	129	12 Q8QVU1	Q8QVU1 hepatitis b
35	42	100.0	129	12 Q8QVU0	Q8QVU0 hepatitis b
36	42	100.0	129	12 Q8QVU5	Q8QVU5 hepatitis b
37	42	100.0	129	12 Q8QVT1	Q8QVT1 hepatitis b
38	42	100.0	129	12 Q8QVU2	Q8QVU2 hepatitis b
39	42	100.0	129	12 Q8QVT3	Q8QVT3 hepatitis b
40	42	100.0	129	12 Q8QVT0	Q8QVT0 hepatitis b
41	42	100.0	129	12 Q8QVT4	Q8QVT4 hepatitis b
42	42	100.0	129	12 Q8QVS9	Q8QVS9 hepatitis b
43	42	100.0	129	12 Q8QVT7	Q8QVT7 hepatitis b
44	42	100.0	129	12 Q8QVT2	Q8QVT2 hepatitis b
45	42	100.0	129	12 Q8QVT6	Q8QVT6 hepatitis b

ALIGNMENTS

RESULT 1
Q9E0Q4 PRELIMINARY; PRT; 58 AA.
AC Q9E0Q4;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]_TaxID=10407;
RP SEQUENCE FROM N.A.
RC STRAIN=BBECO324;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls".
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289966; AAG25271.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6473 MW; 4ED3CAC1351248E2 CRC64;
Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMSTTDLEA 9
Db 6 AMSTTDLEA 14
RESULT 2
Q9E0P6 PRELIMINARY; PRT; 58 AA.
ID Q9E0P6
AC Q9E0P6;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0412;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289970; AAG25279.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 58 AA; 6464 MW; 195CADD94A848F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 3
Q9E0U2 PRELIMINARY; PRT; 58 AA.
AC Q9E0U2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0412;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289970; AAG25279.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 4
Q9E0S4 PRELIMINARY; PRT; 58 AA.
AC Q9E0S4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0138;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289956; AAG25251.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADD84DF48E2 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 5
Q9E0P2 PRELIMINARY; PRT; 58 AA.
AC Q9E0P2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC0380;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289972; AAG25283.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
SQ SEQUENCE 58 AA; 6490 MW; 195CACC1351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 6
Q9E0S6 PRELIMINARY; PRT; 58 AA.
AC Q9E0S6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
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CC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.

CC NCBI_TaxID=10407;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BBSC015;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RL HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289955; AAG25249.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6487 MW; 485DACC1351248E8 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 6 AMSTTDLEA 14

RESULT 7

CC Q9E0U0 PRELIMINARY; PRT; 58 AA.
 AC Q9E0U0;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0148;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RL HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289948; AAG25235.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 6 AMSTTDLEA 14

RESULT 8

CC Q9E0Q2 PRELIMINARY; PRT; 58 AA.
 AC Q9E0Q2;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC053;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;

RP SEQUENCE FROM N.A.

RC STRAIN=BBSC0354;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RL HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289967; AAG25273.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADDE4DF48E2 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 6 AMSTTDLEA 14

RESULT 9

CC Q9E0S2 PRELIMINARY; PRT; 58 AA.
 AC Q9E0S2;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0308;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RL HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289957; AAG25253.1; -;
 DR InterPro: IPR000236; TransactX.
 DR Pfam: PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6494 MW; B8B3BDDDE4DF48FF CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 6 AMSTTDLEA 14

RESULT 10

CC Q9E0W6 PRELIMINARY; PRT; 58 AA.
 AC Q9E0W6;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC053;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;

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RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289935; AAG25209.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6464 MW; 195CACDA94A848F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 11
Q9E0R4 PRELIMINARY; PRT; 58 AA.
AC Q9E0R4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC259;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289961; AAG25261.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 12
Q9E0P0 PRELIMINARY; PRT; 58 AA.
AC Q9E0P0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC399;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289973; AAG25285.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 13
Q9E0V2 PRELIMINARY; PRT; 58 AA.
AC Q9E0V2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC140;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289942; AAG25223.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER
SQ SEQUENCE 58 AA; 6490 MW; 195CACCI351248F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
DB 6 AMSTTDLEA 14

RESULT 14
Q9E0U8 PRELIMINARY; PRT; 58 AA.
AC Q9E0U8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BSHCC180;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289944; AAG25227.1; -.
DR InterPro; IPR000236; TransactX.

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DR Pfam; PF00739; X; 1. 1
FT NON TER 1
SQ SEQUENCE 58 AA; 6506 MW; B65CACC135125E98 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 AMSTTDLEA 9
 |||||
2b 6 AMSTTDLEA 14

RESULT 15
29EOWO PRELIMINARY; PRT; 58 AA.
AC Q9EOWO;
JT 01-MAR-2001 (T-EMBLrel. 16, Created)
JT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
JT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE X protein (Fragment).
EN X.
DS Hepatitis B virus.
DC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
DX NCBI_TaxID=10407;
UN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBHCC64;
UA Tagger A., Binelli G., Donato F., Ribero M.L.;
XT "Prevalence of 1762r and 1764r Mutations in the Basic Core Promoter of
XT HBV Isolated from Patients with Hepatocellular Carcinoma and
XT Controls.";
XT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF28938; AAG25215.1; -
RR InterPro; IPR000236; TransactX.
RR Pfam; PF00739; X; 1. 1
T NON TER 1
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match 100.0%; Score 42; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.084; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 AMSTTDLEA 9
 |||||
b 6 AMSTTDLEA 14

Search completed: December 23, 2003, 08:46:10
Job time : 24.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:41:18 ; Search time 9.6 Seconds
(without alignments)
39.666 Million cell updates/sec

Title: US-09-989-621-4

Perfect score: 55

Sequence: 1 CLFKDWEEL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	4	US-09-051-006-4
2	55	100.0	17	6	5183734-17
3	55	100.0	18	6	5183734-9
4	55	100.0	24	6	5204446-3
5	55	100.0	37	2	US-08-319-376-5
6	55	100.0	154	6	5183734-1
7	52	94.5	24	6	5204446-1
8	52	94.5	24	6	5204446-2
9	52	94.5	153	6	5196194-20
10	52	94.5	154	6	US-09-719-528A-5
11	46	83.6	16	6	5183734-3
12	40	72.7	462	4	US-09-134-001C-3717
13	37	67.3	14	5	PCT-US94-06360-2
14	37	67.3	936	5	PCT-US93-05944-2
15	37	67.3	1008	4	US-09-308-453-2
16	37	67.3	1118	3	US-09-379-523-3
17	36	65.5	307	4	US-09-107-532A-6172
18	36	65.5	334	4	US-09-252-991A-18454
19	35	63.6	587	4	US-09-252-991A-21170
20	35	63.6	1128	4	US-09-328-352-4973
21	35	63.6	1226	4	US-09-601-537-7
22	35	63.6	1227	2	US-08-760-075A-18
23	35	63.6	1227	3	US-09-338-546-18
24	35	63.6	1227	4	US-09-659-084-18
25	34	61.8	141	4	US-09-107-532A-4835
26	34	61.8	209	4	US-09-328-352-7988
27	34	61.8	271	1	US-08-467-155A-10

28	34	61.8	271	2	US-08-628-198-10	Sequence 10, Appl
29	34	61.8	271	3	US-09-201-038-10	Sequence 10, Appl
30	34	61.8	271	5	PCT-US96-07343-10	Sequence 10, Appl
31	34	61.8	286	5	PCT-US92-00282-9	Sequence 9, Appl
32	34	61.8	287	4	US-09-305-856B-10	Sequence 10, Appl
33	34	61.8	630	3	US-08-771-986A-2	Sequence 2, Appl
34	34	61.8	631	4	US-08-769-802A-2	Sequence 2, Appl
35	34	61.8	631	4	US-09-252-991A-26444	Sequence 26444, A
36	34	61.8	752	4	US-09-873-404-2	Sequence 2, Appl
37	34	61.8	752	1	US-08-244-189-2	Sequence 2, Appl
38	34	61.8	823	1	US-08-461-551-2	Sequence 2, Appl
39	34	61.8	823	4	US-09-037-621A-2	Sequence 2, Appl
40	34	61.8	1068	3	US-08-390-874C-11	Sequence 11, Appl
41	34	61.8	1068	4	US-09-265-772-11	Sequence 11, Appl
42	34	61.8	1069	2	US-08-162-081B-37	Sequence 37, Appl
43	34	61.8	1069	3	US-08-780-872-37	Sequence 37, Appl
44	34	61.8	1069	3	US-09-085-957-37	Sequence 37, Appl
45	34	61.8	1080	2	US-08-162-081B-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-09-051-006-4

; Sequence 4, Application US/09051006

; Patent No. 6380359

; GENERAL INFORMATION:

; APPLICANT: Mogam Biotechnology Research Institute

; APPLICANT: Kim, Tae-Young

; APPLICANT: Lee, Ki-Young

; APPLICANT: Chang, Jin-Soo

; APPLICANT: Cho, Sung-Yoo

; APPLICANT: Hwang, Yu-Kyeong

; APPLICANT: Choi, Myeong

; APPLICANT: Cheong, Hong-Seok

; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens

; FILE REFERENCE: 0136/0E154

; CURRENT APPLICATION NUMBER: US/09/051.006

; CURRENT FILING DATE: 1998-03-30

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-09-051-006-4

Query Match 100.0%; Score 55; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. NO 2.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

Db 1 CLFKDWEEL 9

RESULT 2

5183734-17

; Patent No. 5183734

; APPLICANT: MORIARTY, ANN M.

; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS

; FOR ASSAYING SV40 HEXAG

; NUMBER OF SEQUENCES: 17

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/553,982

; FILING DATE: 17-JUL-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 54,424

; FILING DATE: 26-MAY-1987

; APPLICATION NUMBER: 648,142

; FILING DATE: 07-SEP-1984

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; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:17:
; LENGTH: 17
5183734-17
Query Match      100.0%; Score 55; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 1 CLFKDWEEL 9

RESULT 3
5183734-9
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:9:
; LENGTH: 18
5183734-9
Query Match      100.0%; Score 55; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 1 CLFKDWEEL 9

RESULT 4
5204446-3
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIAKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:3:
; LENGTH: 24
5204446-3
Query Match      100.0%; Score 55; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 2 CLFKDWEEL 10

RESULT 5
US-08-319-376-5
; Sequence 5, Application US/08319376
; Patent No. 5872205
; GENERAL INFORMATION:
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:1:
; LENGTH: 154
5183734-1
Query Match      100.0%; Score 55; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: Liang, Tsanyang J
; APPLICANT: Huang, Jiakang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INTERFERING
; WITH INFECTION: WITH HEPATITIS B VIRUS INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,376
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: MGH-126XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-319-376-5
Query Match      100.0%; Score 55; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 5 CLFKDWEEL 13

RESULT 6
5183734-1
; Patent No. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HBXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:1:
; LENGTH: 154
5183734-1
Query Match      100.0%; Score 55; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CLFKDWEEL 9
Db 115 CVFKDWEEL 123

RESULT 7
5204446-1
;PATENT NO. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI,OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:1:
; LENGTH: 24
5204446-1

Query Match 94.5%; Score 52; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 2 CVFKDWEEL 10

RESULT 8
5204446-2
;PATENT NO. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI,OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:2:
; LENGTH: 24
5204446-2

Query Match 94.5%; Score 52; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 2 CVFKDWEEL 10

RESULT 9
5196194-20
;PATENT NO. 5196194
; APPLICANT: RUTTER, WILLIAM J.;GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:20:
; LENGTH: 153
5196194-20

Query Match 94.5%; Score 52; DB 6; Length 153;

Best Local Similarity 88.9%; Pred. No. 0.09;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLFKDWEEL 9
Db 115 CVFKDWEEL 123

RESULT 10
US-09-719-528A-5
; Sequence 5, Application US/09719528A
; Patent No. 6586675
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00045
FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-719-528A-5

Query Match 94.5%; Score 52; DB 4; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.091;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
Db 115 CVFKDWEEL 123

RESULT 11
5183734-3
;PATENT NO. 5183734
; APPLICANT: MORIARTY, ANN M.
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
; FOR ASSAYING SV40 HEXAG
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,982
; FILING DATE: 17-JUL-1990


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 54,424
; FILING DATE: 26-MAY-1987
; APPLICATION NUMBER: 648,142
; FILING DATE: 07-SEP-1984
; APPLICATION NUMBER: 587,570
; FILING DATE: 08-MAR-1984
; SEQ ID NO:3
; LENGTH: 16
; 5183734-3

Query Match      83.6%; Score 46; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.092; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LFKDWEEL 9
Db      1 LFKDWEEL 8
        |||||
        |||||

RESULT 12
US-09-134-001C-3717
; Sequence 3717, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3717
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3717

Query Match      72.7%; Score 40; DB 4; Length 462;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LFKDWEEL 9
Db      88 IFKDWEKL 95
        :|||:
        :|||:

RESULT 13
PCT-US94-06360-2
; Sequence 2, Application PC/TUS9406360
; GENERAL INFORMATION:
; APPLICANT: Mark Feitelson
; TITLE OF INVENTION: Method of Detecting Hepatitis B Variants
; TITLE OF INVENTION: Having Deletions Within the X Region of the Virus Genome
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06360

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; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,346
; FILING DATE: June 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
PCT-US94-06360-2

Query Match      67.3%; Score 37; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LFKDWE 7
Db      1 LFKDWE 6
        |||||
        |||||

RESULT 14
PCT-US93-05944-2
; Sequence 2, Application PC/TUS9305944
; GENERAL INFORMATION:
; APPLICANT: Lin et al., Hun-Chi
; TITLE OF INVENTION: Molecular cloning of the genes
; TITLE OF INVENTION: responsible for collagenase product
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harris Brotman
; STREET: 401 B. St Ste 1700
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05944
; FILING DATE: 19930622
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brotman, Harris F.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-3630
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-05944-2

Query Match      67.3%; Score 37; DB 5; Length 936;
Best Local Similarity 71.4%; Pred. No. 28+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      3 FKDWEEL 9
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Db 551 FKDWDEM 557

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RESULT 15
US-09-308-453-2
; Sequence 2, Application US/09308453
; Patent No. 6475764
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GMBH
; TITLE OF INVENTION: Recombinant collagenase type I from Clostridium histolyticum and
; TITLE OF INVENTION: for isolating cells and groups of cells
; FILE REFERENCE: BMID9924US
; CURRENT APPLICATION NUMBER: US/09/308,453
; NUMBER OF SEQ ID NOS: 24
; CURRENT FILING DATE: 1999-09-09
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: Clostridium histolyticum
US-09-308-453-2

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Query Match 67.3%; Score 37; DB 4; Length 1008;
 Best Local Similarity 71.4%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

2y 3 FKDWEEEL 9
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 Db 623 FKDWDEM 629

Search completed: December 23, 2003, 08:53:50
 Job time : 10.6 secs

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	55	100.0	9	10	US-09-989-621-4	Sequence 4, Appli
	2	52	94.5	154	15	US-10-209-264-5	Sequence 5, Appli
	3	43	78.2	1146	9	US-09-815-242-11211	Sequence 11211, A
	4	36	65.5	283	9	US-09-925-299-984	Sequence 984, App
	5	36	65.5	283	11	US-09-925-299-984	Sequence 984, App
	6	36	65.5	316	12	US-09-907-218-76	Sequence 76, Appl
	7	36	65.5	316	12	US-10-387-629-120	Sequence 120, App
	8	36	65.5	620	15	US-10-156-761-14439	Sequence 14439, A
	9	35	63.6	26	10	US-09-984-245-150	Sequence 150, App
	10	35	63.6	26	11	US-09-966-262-150	Sequence 150, App
	11	35	63.6	26	11	US-09-983-965-150	Sequence 150, App
	12	35	63.6	26	15	US-10-143-090-150	Sequence 150, App
	13	35	63.6	107	9	US-09-864-761-43456	Sequence 43456, A
	14	34.5	62.7	84	12	US-10-340-578-57	Sequence 57, Appl
	15	34	61.8	219	12	US-10-223-081-332	Sequence 332, App

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US-10-209-264-5
; Sequence 5, Application US/10209264
; Publication No. US2003003111A1
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
;             Lim, Gek Keow
;             Zhao, Yi
;             Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
;                   USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Ladas & Parry
;             STREET: 26 West 61 Street
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/209,264
; FILING DATE: 31-Jul-2002
; CLASSIFICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SG98/00046
; FILING DATE: 19-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-013109-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-209-264-5
Query Match          94.5%; Score 52; DB 15; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
Db      115 CVFKDWEEL 123

RESULT 3
US-09-815-242-11211
; Sequence 11211, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11211
; LENGTH: 1146
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11211
Query Match          78.2%; Score 43; DB 9; Length 1146;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
Db      69 CLFPDWETL 77

RESULT 4
US-09-925-299-984
; Sequence 984, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 984
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (268)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-984
Query Match          65.5%; Score 36; DB 9; Length 283;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CLFKDWE 7
Db      114 CLFKDWE 120

RESULT 5
US-09-925-299-984
; Sequence 984, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA102
 ; CURRENT APPLICATION NUMBER: US/09/925,299
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05863
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1998-03-12
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 984
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (103)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (268)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-925-299-984

Query Match 65.5%; Score 36; DB 11; Length 283;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLFKDWE 7
 DB 114 CLFKDWE 120

RESULT 6
 US-09-907-218-76
 ; Sequence 76, Application US/09907218
 ; Publication No. US20030168645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigar, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Tailon, Bruce
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Wolenc, Adam Ryan
 ; APPLICANT: Li, Li
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly Ann
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-061
 ; CURRENT APPLICATION NUMBER: US/09/907,218
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: 60/218,746
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 60/260,977
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 60/263,801
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: 60/268,226
 ; PRIOR FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/271,622
 ; PRIOR FILING DATE: 2001-02-26
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 76
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-907-218-76

Query Match 65.5%; Score 36; DB 12; Length 316;
 Best Local Similarity 71.4%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFKDWE 8
 DB 308 LFKDWE 314

RESULT 7
 US-10-387-629-120
 ; Sequence 120, Application US/10387629
 ; Publication No. US20030221205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChemCom S.A.
 ; APPLICANT: Veithen, Alex
 ; TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
 ; FILE REFERENCE: 9409/2192
 ; CURRENT APPLICATION NUMBER: US/10/387,629
 ; CURRENT FILING DATE: 2003-03-13
 ; NUMBER OF SEQ ID NOS: 254
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 120
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-387-629-120

Query Match 65.5%; Score 36; DB 12; Length 316;
 Best Local Similarity 71.4%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFKDWE 8
 DB 308 LFKDWE 314

RESULT 8
 US-10-156-761-14439
 ; Sequence 14439, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 14439
 ; LENGTH: 620
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 ; US-10-156-761-14439

Query Match 65.5%; Score 36; DB 15; Length 620;
 Best Local Similarity 75.0%; Pred. No. 5.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFKDWE 9
 DB 147 LFKDWE 154

RESULT 9
 US-09-984-245-150
 ; Sequence 150, Application US/09984245
 ; Patent No. US20020165374A1

GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-150

Query Match 63.6%; Score 35; DB 10; Length 26;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LFKDWEEL 9
Db 4 IPEWENL 11

RESULT 10
US-09-966-262-150
; Sequence 150, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-150

Query Match 63.6%; Score 35; DB 11; Length 26;

Best Local Similarity 62.5%; Score 35; DB 11; Length 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LFKDWEEL 9
Db 4 IFKEWENL 11
RESULT 11
US-09-983-966-150
; Sequence 150, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 150

LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-150
Query Match 63.6%; Score 35; DB 11; Length 26;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LFKDWEEL 9
Db 4 IFKEWENL 11
RESULT 12
US-10-143-090-150
; Sequence 150, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 150
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-090-150
Query Match 63.6%; Score 35; DB 15; Length 26;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LFKDWEEL 9
Db 4 IFKEWENL 11
RESULT 13
US-09-864-761-43456
; Sequence 43456, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43456
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004682.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EST HUMAN HIT: BF182859.1, EVALUE 1.1
; OTHER INFORMATION: SWISSPROT HIT: Q92620, EVALUE 1.00e-35
US-09-864-761-43456

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Query Match      63.6%; Score 35; DB 9; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      3 PKDWE 8
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Db      79 YKDWE 84

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RESULT 14
US-10-340-578-57
; Sequence 57, Application US/10340578
; Publication No. US20030153097A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: DESHAIES, Raymond J.
; APPLICANT: COPE, Gregory
; APPLICANT: VERMA, Rati
; APPLICANT: AMBROGGIO, Xavier J.
; TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
; FILE REFERENCE: CITI590-1.
; CURRENT APPLICATION NUMBER: US/10/340,578
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/355,334
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 10/047,253
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 10/046,961
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/322,322
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,030
; PRIOR FILING DATE: 2001-09-14

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; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Ralstonia solanacearum
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (41)..(41)
; OTHER INFORMATION: Xaa indicates 18 amino acid residues
US-10-340-578-57

Query Match      62.7%; Score 34.5; DB 12; Length 84;
Best Local Similarity 50.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY      1 CLFKD-----WEEL 9
        :|||||
Db      23 CLFLDYRHRLIAWEEL 38

RESULT 15
US-10-223-081-332
; Sequence 332, Application US/10223081
; Publication No. US2003018686A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC7
; CURRENT APPLICATION NUMBER: US/10/223,081
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 332
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-081-332

```


Query Match 61.8%; Score 34; DB 12; Length 219;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Cy 2 LFXDWHEEL 9
Db 126 LFKWQDM 133

Search completed: December 23, 2003, 08:52:50
Job time : 80.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-4

Perfect score: 55

Sequence: 1 CLFKDWEEL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	134	1 B49345	gene X protein, tr
2	55	100.0	154	1 QVLD1	gene X protein - h
3	55	100.0	154	1 QVLD1	gene X protein - h
4	55	100.0	154	1 QVLD1	gene X protein - h
5	55	100.0	154	1 A48345	gene X protein - h
6	55	100.0	154	2 S47404	gene X protein - h
7	55	100.0	154	2 S3130	gene X protein - h
8	55	100.0	154	2 S3529	gene X protein - h
9	55	100.0	154	2 T13466	gene X protein - h
10	55	100.0	210	2 S12598	gene X protein - h
11	52	94.5	154	1 QVLD1	gene X protein - h
12	52	94.5	154	1 QVLD1	gene X protein - h
13	52	94.5	154	1 QVLD1	gene X protein - h
14	52	94.5	154	2 S20756	gene X protein - h
15	52	94.5	154	2 S47408	gene X protein - h
16	52	94.5	154	2 J02228	trans-activating p
17	52	94.5	154	2 S25650	gene X protein - h
18	52	94.5	154	2 S3687	gene X protein - h
19	52	94.5	154	2 S2542	gene X protein - h
20	52	94.5	154	2 S20751	gene X protein - h
21	52	94.5	172	2 A58456	gene X protein - h
22	52	94.5	359	2 S04570	gene X/C fusion pr
23	51	92.7	154	1 QVLD1	gene X protein - h
24	51	92.7	154	2 S2319	gene X protein - h
25	51	92.7	210	2 T13472	gene X protein - h
26	48	87.3	154	2 S67503	gene X protein - h
27	43	78.2	154	2 S0256	gene X protein - h
28	43	78.2	154	2 J80603	gene X protein - h
29	43	79.2	1146	1 I64112	transcription/rep

ALIGNMENTS

RESULT 1

B48345

gene X protein, truncated form - hepatitis B virus

C/Species: hepatitis B virus, HBV

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C/Accession: B48345

R/Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert, Arch. Virol. 125, 299-304, 1992

A/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer I

A/Reference number: A48345; MUID:92352333; PMID:1642555

A/Accession: B48345

A/Molecule type: DNA

A/Residues: 1-134 <REP>

A/Cross-references: GB:S41176; NID:9252541; PIDN:AAB22733.1; PID:3252542

A/Note: sequence extracted from NCBI backbone (NCBI:109914, NCBIP:109915)

C/Genetics:

A/Gene: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

DB 115 CLFKDWEEL 123

RESULT 2

QVLD1

gene X protein - hepatitis B virus (subtype ayw)

C/Species: hepatitis B virus, HBV

C/Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Apr-1994

C/Accession: A03719

R/Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.

A/Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A/Reference number: A93214; MUID:81012891; PMID:399327

A/Accession: A03719

A/Molecule type: DNA

A/Residues: 1-154 <GAL>

A/Cross-references: GB:J02203; GB:V01460

C/Genetics:

A/Gene: X

C/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

DB 115 CLFKDWEEL 123

gene X protein - h
hypothetical prote
hypothetical prote
penicillin-binding
trypsin (EC 3.4.21
hypothetical prote
T24D18.25 protein
response regulator
hypothetical prote
probable phage pro
peptide synthetase
conserved hypothet
DNA helicase relat
microcystin synthe
hypothetical prote
hypothetical prote

```

Db      115 CLFKDWEEL 123

RESULT 3
QQVIBH
Gene X protein - hepatitis B virus (subtype ayw, strain PHB320)
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, strain PHB320
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Jul-2000
C/Accession: A05237; S53144; S53173; S53195; S53210; S53222; S53224; S53235; S53280
R/Bichko, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985
A/Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A/Reference number: A05237; PMID:83204397; PMID:3996597
A/Accession: A05237
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-154 <BIG>
A/Cross-references: EMBL:X02496; NID:G62280; PIDN:CA841697.1; PID:G4704317
R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53112
A/Accession: S53144
A/Molecule type: DNA
A/Residues: 124-154 <LA1>
A/Cross-references: EMBL:X85267; NID:G736025; PIDN:CAA59548.1; PID:G736026; EMBL:X85284;
S5305; EMBL:X83307; EMBL:X83308; EMBL:X85310; EMBL:X85312; EMBL:X85315; EMBL:
A/Experimental source: isolate patient Pintus/85 et al.
A/Accession: S53173
A/Molecule type: DNA
A/Residues: 124-154 <LA2>
A/Cross-references: EMBL:X85277; NID:G736065; PIDN:CAA59575.1; PID:G736066
A/Experimental source: isolate patient Bio'90
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 4
A48345
Gene X protein - hepatitis B virus
C/Species: hepatitis B virus, HBV
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C/Accession: A48345
R/Repp, R.; Keller, C.; Borkhardt, A.; Caecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,
Arch. Virol. 125, 299-304, 1992
A/Title: Detection of a hepatitis B virus variant with a truncated x gene and enhancer I
A/Reference number: A48345; PMID:92352333; PMID:1642555
A/Accession: A48345
A/Molecule type: DNA
A/Residues: 1-154 <REP>
A/Cross-references: GB:S41175; NID:G252539; PIDN:ABA22732.1; PID:G252540
A/Note: sequence extracted from NCBI backbone (NCBIN:109912, NCBI:P109913)
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 5
S47404
Gene X protein - hepatitis B virus (subtype ayw4)
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw4
C/Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C/Accession: S47404
R/Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A/Description: Molecular cloning and sequencing of two complete genomes of polish isola
A/Reference number: S47404
A/Accession: S47404
A/Molecule type: DNA
A/Residues: 1-154 <PLU>
A/Cross-references: EMBL:X35716; NID:G527435; PIDN:CAA84785.1; PID:G527436
A/Experimental source: subtype ayw4
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 6
S53130
Gene X protein - hepatitis B virus
C/Species: hepatitis B virus, HBV
C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C/Accession: S53130
R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53112
A/Accession: S53130
A/Molecule type: DNA
A/Residues: 1-154 <LA1>
A/Cross-references: EMBL:X85254; NID:G736003; PIDN:CAA59513.1; PID:G736007
C/Genetics:
A/Gene: X
C/Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      |||||
Db      115 CLFKDWEEL 123

RESULT 7
S35529
Gene X protein - hepatitis B virus (subtype adr)
C/Species: hepatitis B virus, HBV
A/Variety: subtype adr
C/Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C/Accession: S35529
R/Mukaide, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hiki, K.
Nucleic Acids Res. 20, 6105, 1992
A/Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and
A/Reference number: S35527; PMID:93096607; PMID:11461746
A/Accession: S35529
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-154 <MUK>

```

```

A;Cross-references: EMBL:D12980; NID:g221500; PIDN:BAA02356.1; PID:g221503
A;Experimental source: subtype adr
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
    |||||
Db 115 CLFKDWEEL 123

RESULT 8
S32203
gene X protein - hepatitis B virus (subtype ayw, patient C1000)
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient C1000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S32203
R;Pretzler-Adams, S.; Schlager, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
A;Description: Identification and sequence analysis of hepatitis B virus DNA in immunolod
A;Reference number: S32202
A;Accession: S32203
A;Molecule type: DNA
A;Residues: 1-154 <PRE>
A;Cross-references: EMBL:X72702; NID:g288927; PIDN:CAAS1256.1; PID:g288929
A;Experimental source: subtype ayw, patient C1000
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
    |||||
Db 115 CLFKDWEEL 123

RESULT 9
T13466
gene X protein - hepatitis B virus (isolate 09D09HCC)
C;Species: hepatitis B virus, HBV
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: T13466
R;Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishiho, S.
Arch. Virol. 143, 2313-2326, 1998
A;Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin
A;Reference number: Z17684; MUID:99129050; PMID:9930189
A;Accession: T13466
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-154 <TA>
A;Cross-references: EMBL:AB014368; NID:g3551304; PIDN:BAA32861.2; PID:g6116706
A;Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HCC
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
    |||||
Db 115 CLFKDWEEL 123

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RESULT 10
S12598
gene X protein - hepatitis B virus (subtype adr)
N;Contains: pre-X domain
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 13-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
R;Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
Nucleic Acids Res. 18, 4940, 1990
A;Title: Sequence of a replication competent hepatitis B virus genome with a preX open ;
A;Reference number: S12598; MUID:90370503; PMID:2395664
A;Accession: S12598
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-210 <LON>
A;Cross-references: EMBL:X52939
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 55; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
    |||||
Db 171 CLFKDWEEL 179

RESULT 11
QOVLAW
gene X protein - hepatitis B virus (subtype adw and adw2)
C;Species: hepatitis B virus, HBV
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998
C;Accession: A31289; B94409; A03719
R;Lo, S.J.; Chien, M.L.; Lee, Y.H.W.
Virology 167, 289-292, 1988
A;Title: Characteristics of the X gene of hepatitis B virus.
A;Reference number: A31289; MUID:89045656; PMID:3188399
A;Accession: A31289
A;Molecule type: DNA
A;Residues: 1-154 <LOS>
A;Experimental source: subtype adw
R;Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad
A;Reference number: A94409
A;Accession: B94409
A;Molecule type: DNA
A;Residues: 1-154 <VAL>
A;Experimental source: subtype adw2
C;Genetics:
A;Gene: X
C;Superfamily: hepatitis B virus gene X protein

Query Match      94.5%; Score 52; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.056;
Matches          8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
    |||||
Db 115 CVFKDWEEL 123

RESULT 12
QOVLKS
gene X protein - hepatitis B virus (subtype adw, strain 991)
C;Species: hepatitis B virus, HBV
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S10380
R;Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.
submitted to the EMBL Data Library, February 1990

```

A;Reference number: S10380
 A;Accession: S10380
 A;Molecule type: DNA
 A;Residues: 1-154 <KOE>
 A;Cross-references: EMBL:X51970; NID:G1155012; PIDN:CAA36231.1; PID:G60432
 C;Genetics:
 A;Gene: X
 C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 1; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CLFKDWHEEL 9
 :|||||
 Db 115 CVFKDWHEEL 123

RESULT 13

QOVLCP
 gene X protein - hepatitis B virus (strain LSH, chimpanzee)

C;Species: hepatitis B virus, HBV
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
 C;Accession: D28885

R;Vaudin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.

J. Gen. Virol. 69, 1383-1389, 1988

A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated

A;Reference number: A92796; MUID:88258473; PMID:2838576

A;Accession: D28885

A;Molecule type: DNA

A;Residues: 1-154 <VAU>

A;Cross-references: GB:D00220; NID:G221505; PIDN:BAA00160.1; PID:G221509

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 1; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CLFKDWHEEL 9
 :|||||
 Db 115 CVFKDWHEEL 123

RESULT 14

S20756

gene X protein - hepatitis B virus (subtype ayw, patient E)

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw, patient E

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;Accession: S20756

R;Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.

submitted to the EMBL Data Library, March 1992

A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati

A;Reference number: S20745

A;Accession: S20756

A;Molecule type: DNA

A;Residues: 1-154 <LAI>

A;Cross-references: EMBL:X65259; NID:G59439; PIDN:CAA46360.1; PID:G59443

A;Experimental source: subtype ayw, patient E

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 2; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CLFKDWHEEL 9
 :|||||
 Db 115 CVFKDWHEEL 123

RESULT 15

S47408

gene X protein - hepatitis B virus (subtype adw2)

C;Species: hepatitis B virus, HBV

A;Variety: subtype adw2

C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999

C;Accession: S47408

R;Plucienniczak, A.

submitted to the EMBL Data Library, August 1994

A;Description: Molecular cloning and sequencing of two complete genomes of polish isola

A;Reference number: S47404

A;Accession: S47408

A;Molecule type: DNA

A;Residues: 1-154 <PLU>

A;Cross-references: EMBL:Z35717; NID:G527440; PIDN:CAA84789.1; PID:G527441

A;Experimental source: subtype adw2

C;Genetics:

A;Gene: X

C;Superfamily: hepatitis B virus gene X protein

Query Match 94.5%; Score 52; DB 2; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.056;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CLFKDWHEEL 9
 :|||||
 Db 115 CVFKDWHEEL 123

Search completed: December 23, 2003, 08:41:09

Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 Seconds
(without alignments) updates/sec
66.131 Million cell

Title: US-09-989-621-4
Perfect score: 55
Sequence: 1 CLFKDWEEL 9

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	55	100.0	154	1 X HPEV4	P12936 hepatitis b
2	55	100.0	154	1 X HPEV4	P03165 hepatitis b
3	52	94.5	154	1 X HPEV2	P03165 hepatitis b
4	52	94.5	154	1 X HPEV2	P17102 hepatitis b
5	52	94.5	154	1 X HPEV4	P12912 hepatitis b
6	52	94.5	154	1 X HPEV4	Q05499 hepatitis b
7	51	92.7	154	1 X HPEV4	P24026 hepatitis b
8	43	78.2	154	1 X HPEV4	P20976 hepatitis b
9	43	78.2	154	1 X HPEV4	P20977 hepatitis b
10	43	78.2	154	1 X HPEV4	P45128 haemophilus
11	42	76.4	154	1 X HPEV4	P20975 hepatitis b
12	42	76.4	154	1 X HPEV4	O59025 pyrococcus
13	38	69.1	1023	1 DPO2_ADEB3	O72540 bovine aden
14	37	67.3	1715	1 HELS_PIRAB	Q9V049 pyrococcus
15	37	67.3	1756	1 YCF1_PINTH	P41647 pinus thunb
16	36	65.5	316	1 YCF1_PINTH	Q9UGF7 homo sapien
17	36	65.5	347	1 VIPL_MOUSE	P59481 mus musculu
18	36	65.5	354	1 AROC_BUCAI	P57198 buchnera ap
19	36	65.5	356	1 VP36_CANFA	P49256 canis famil
20	36	65.5	356	1 VP36_HUMAN	Q12907 homo sapien
21	36	65.5	358	1 VP36_MOUSE	Q9DBH5 mus musculu
22	36	65.5	607	1 PRIM_MYCSE	P47432 mycoplasma
23	36	65.5	620	1 PRIM_MYCSE	P75426 mycoplasma
24	36	65.5	704	1 HELS_SULTO	Q97481 sulfolobus
25	35	63.6	311	1 FNPH_YEAST	Q05788 saccharomyc
26	35	63.6	353	1 AROC_BUCAP	Q9ZHE9 buchnera ap
27	35	63.6	413	1 YGSO_YEAST	P45819 saccharomyc
28	35	63.6	484	1 AMYA_ASPNG	P56271 aspergillus
29	35	63.6	662	1 HEPA_HSV6U	P52375 human herpe
30	35	63.6	662	1 HEPA_HSV6U	P52451 human herpe
31	35	63.6	708	1 HELS_SULTO	Q97W99 sulfolobus
32	35	63.6	879	1 GUN1_CLOTID	Q02934 clostridium
33	35	63.6	880	1 YVL7_CABEL	Q21534 caenorhabdi

RESULT 1

X_HPEV4 STANDARD; PRT; 154 AA.

AC P12936;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Trans-activating protein X.

GN X.

OS Hepatitis B virus (subtype adr4).

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10409;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83246570; PubMed=6306594;

RA Fujiyama A., Miyanchara A., Nozaki C., Yoneyama T., Ohtomo N.,

RA Matsubara K.,

RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype

RT adr4";

RL Nucleic Acids Res. 11:4601-4610(1983).

CC - FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----

CC EMBL; X01587; CAA25744.1; -

CC InterPro; IPR000236; TransactX.

CC Pfam; PF00739; X; 1.

CC SEQUENCE 154 AA; 16622 MW; 594A1D0716928804 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.0052;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

DB 115 CLFKDWEEL 123

RESULT 2

X_HPEV4 STANDARD; PRT; 154 AA.

AC P03165;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Trans-activating protein X.

GN X.

OS Hepatitis B virus (subtype ayw).

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10418;

Q92620 homo sapien
Q8XW10 ralestonia s
P40347 saccharomyc
P35032 salmo salar
Q9K115 bacillus ha
Q58216 methanococc
P70662 mus musculu
P70060 xenopus lae
P38953 saccharomyc
P18162 tipula irid
P22166 simulium ir

ALIGNMENTS

```

RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81012091; PubMed=399327;
RA  Galibert F., Mandart E., Fickoussi F., Tiollais P., Charnay P.;
RT  "Nucleotide sequence of the hepatitis B virus genome (subtype a/yw)
RL  cloned in E. coli.";
RL  Nature 281:646-650 (1979).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85204397; PubMed=3956597;
RA  Bichko V., Drailina D., Pushko P.M., Pumpen P.P., Gren E.;
RT  "Subtype a/yw variant of hepatitis B virus. DNA primary structure
RT  analysis.";
RL  FEBS Lett. 185:208-212 (1985).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85204397; PubMed=3956597;
RA  Bichko V., Drailina D., Pushko P.M., Pumpen P.P., Gren E.;
RT  "Subtype a/yw variant of hepatitis B virus. DNA primary structure
RT  analysis.";
RL  FEBS Lett. 185:208-212 (1985).
CC  -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
DR  EMBL; V01460; -; NOT_ANNOTATED_CDS.
DR  EMBL; X02496; CAB41697.1; -.
DR  PIR; A03719; QOVLDI.
DR  PIR; A05237; QOVLBH.
DR  InterPro; IPR000236; TransactX.
DR  Pfam; PF00739; X; 1.
FT  VARIANT 46 46 P -> S (IN STRAIN LATVIA).
FT  VARIANT 84 88 NAHQI -> KAQPF (IN STRAIN LATVIA).
FT  VARIANT 102 102 A -> V (IN STRAIN LATVIA).
FT  CONFLICT 26 26 R -> C (IN REF. 1).
SQ  SEQUENCE 154 AA; 16618 MW; 29FD1CC9E09A34B5 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLFKDWEEL 9
DB 115 CLFKDWEEL 123
RESULT 3
X_HPBV2
ID X_HPBV2 STANDARD; PRT; 154 AA.
AC P03166; P12935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw2), and
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC NCB1_TaxID=10408, 106821;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RA Valenzuela P., Quiroga M., Zaidivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RA Lo S.J., Chien M.L., Lee Y.H.W.;
RT "Characteristics of the X gene of hepatitis B virus.";
RL Virology 167:289-292 (1988).
RN [3]

```

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RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RA MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757 (1983).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=ADW;
RA MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757 (1983).
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CC or send an email to license@isb-sib.ch).
DR EMBL; X02763; CAA36540.1; -.
DR EMBL; Z35717; CAA84789.1; -.
DR EMBL; M23692; AAA56820.1; -.
DR EMBL; V00866; -; NOT_ANNOTATED_CDS.
DR PIR; A31289; QOVLAW.
DR PIR; S47408; S47408.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT CONFLICT 80 80 E -> A (IN REF. 3).
FT CONFLICT 115 115 C -> S (IN REF. 2).
FT CONFLICT 130 131 KV -> MI (IN REF. 3).
SQ SEQUENCE 154 AA; 16583 MW; 7F2AE32A4F025670 CRC64;
Query Match 94.5%; Score 52; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLFKDWEEL 9
DB 115 CLFKDWEEL 123
RESULT 4
X_HPBV9
ID X_HPBV9 STANDARD; PRT; 154 AA.
AC P17102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC NCB1_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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DR EMBL; X51970; CAA36231.1; -.
DR PIR; S10380; QOVLKS.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16553 MW; 52A0D9CEFE6DCDE0 CRC64;
Query Match 94.5%; Score 52; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.018;

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Matches      8;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 CLFKDWEEL 9
      115 CVFKDWEEL 123

Db

RESULT 5
X_HPBVL
ID      X_HPBVL      STANDARD;      PRT;      154 AA.
AC      P12912;
DT      01-OCT-1989 (Rel. 12, Created)
DT      01-OCT-1989 (Rel. 12, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      Trans-activating protein X.
GN      X.
OS      Hepatitis B virus (strain lsh / chimpanzee isolate).
OC      Viruses; Retrov. viruses; Hepadnaviridae; Orthohepadnavirus.
OX      NCBI_TaxID=10414;
RN      [1].
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88258473; PubMed=2838576;
RA      Vaadin M., Wolstenholme A.J., Taiquaye K.N., Zuckerman A.J.,
RA      Harrison T.J.;
RT      "The complete nucleotide sequence of the genome of a hepatitis B
RT      virus isolated from a naturally infected chimpanzee."
RL      J. Gen. Virol. 69:1383-1389(1988).
CC      -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC      EMBL; D00220; BAA00160.1; -
CC      PIR; D28885; QQVLCF.
CC      InterPro; IPR000236; TransactX.
CC      Pfam; PF00739; X; 1.
CC      SEQUENCE 154 AA; 16759 MW; F6C9D7D30C16D743 CRC64;
CC
CC      Query Match
CC      Best Local Similarity 94.5%; Score 52; DB 1; Length 154;
CC      Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      115 CVFKDWEEL 123

Db

RESULT 6
X_HPBVT
ID      X_HPBVT      STANDARD;      PRT;      154 AA.
AC      Q05499;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      Trans-activating protein X.
GN      X.
OS      Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC      Viruses; Retrov. viruses; Hepadnaviridae; Orthohepadnavirus.
OX      NCBI_TaxID=45410;
RN      [1].
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93346970; PubMed=8345355;
RA      Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA      Gerlich W.H.;
RT      "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT      that expresses HBV surface antigen subtype adw4."
RL      J. Gen. Virol. 74:1627-1632(1993).
CC      -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC
CC      EMBL; X69798; CAA49453.1; -
CC      PIR; JQ2228; JQ2228.
CC      InterPro; IPR000236; TransactX.
CC      Pfam; PF00739; X; 1.
CC      SEQUENCE 154 AA; 16715 MW; E523C051B9B0B737 CRC64;
CC
CC      Query Match
CC      Best Local Similarity 94.5%; Score 52; DB 1; Length 154;
CC      Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 9
      115 CVFKDWEEL 123

Db

RESULT 7
X_HPBVA
ID      X_HPBVA      STANDARD;      PRT;      154 AA.
AC      P24026;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-MAR-1992 (Rel. 21, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      Trans-activating protein X.
GN      X.
OS      Hepatitis B virus (strain alpha1).
OC      Viruses; Retrov. viruses; Hepadnaviridae; Orthohepadnavirus.
OX      NCBI_TaxID=10411;
RN      [1].
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90266476; PubMed=2345966;
RA      Tong S., Li J., Vitvitski L., Trepo C.;
RT      "Active hepatitis B virus replication in the presence of anti-HBe is
RT      associated with viral variants containing an inactive pre-C region."
RL      Virology 176:596-603(1990).
CC      -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC      or send an email to license@isb-sib.ch)
CC
CC      EMBL; M32138; AAA45504.1; -
CC      PIR; D34773; QQVLA1.
CC      InterPro; IPR000236; TransactX.
CC      Pfam; PF00739; X; 1.
CC      SEQUENCE 154 AA; 16671 MW; 2CFEEA77FA5E271F CRC64;
CC
CC      Query Match
CC      Best Local Similarity 92.7%; Score 51; DB 1; Length 154;
CC      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLFKDWEEL 8
      115 CVFKDWEEL 122

Db

RESULT 8
X_HPBVJ
ID      X_HPBVJ      STANDARD;      PRT;      154 AA.
AC      P20976;
DT      01-FEB-1991 (Rel. 17, Created)

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DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Japan/pJDM233).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Saetsoewignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 CC EMBL; D00330; -; NOT ANNOTATED_CDS.
 DR PIR; JS0256; JS0256.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16595 MW; 512A5A077169D5CA CRC64;
 Query Match 78.2%; Score 43; DB 1; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLFQWHEEL 9
 Db 115 CVFNEWHEEL 123

RESULT 9
 X HPBVO
 ID X HPBVO STANDARD; PRT; 154 AA.
 AC P20977;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Saetsoewignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC EMBL; D00330; -; NOT ANNOTATED_CDS.
 DR PIR; JS0603; JS0603.
 DR InterPro; IPR000236; TransactX.

DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;
 Query Match 78.2%; Score 43; DB 1; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLFQWHEEL 9
 Db 115 CVFNEWHEEL 123

RESULT 10
 MFD_HABIN
 ID MFD_HABIN STANDARD; PRT; 1146 AA.
 AC P45128;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription-repair coupling factor (TRCF).
 GN MFD OR H11258.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kervaege A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: NECESSARY FOR STRAND-SPECIFIC REPAIR. A LESION IN THE
 CC TEMPLATE STRAND BLOCKS THE RNA POLYMERASE COMPLEX (RNAP). THE
 CC RNAP-DNA-RNA COMPLEX IS SPECIFICALLY RECOGNIZED BY TRCF WHICH
 CC RELEASES RNAP AND THE TRUNCATED TRANSCRIPT; THE TRCF MAY REPLACE
 CC RNAP AT THE LESION SITE AND THEN RECRUIT THE UVRB/B/C REPAIR
 CC SYSTEM (BY SIMILARITY).
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE UVRB FAMILY.
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE HELICASE
 CC FAMILY. RECG SUBFAMILY.
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 CC
 CC EMBL; U32805; AAC222905.1; -;
 DR PIR; I64112; I64112.
 DR TIGR; H11258; -;
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR004576; Mfd.
 DR InterPro; IPR005118; TRCF.
 DR Pfam; PF02559; Card_TRCF; 1.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF03461; TRCF; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICCC; 1.
 DR TIGRFAMs; TIGR00580; mfd; 1.

KW Helicase; DNA repair; ATP-binding; DNA-binding; Complete proteome.
 FT DOMAIN 600 970 HELICASE; RECG-LIKE.
 FT NP BIND 630 637 ATP (POTENTIAL).
 FT SITE 731 734 DEEH BOX.
 SQ SEQUENCE 1146 AA; 130130 MW; 6E3052BA31978475 CRC64;

Query Match 78.2%; Score 43; DB 1; Length 1146;
 Best Local Similarity 77.8%; Pred. No. 6.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLFQWHEEL 9
 ||| |||||
 Db 69 CLFQWHEEL 77

RESULT 11

X HPBVI STANDARD; PRT; 154 AA.
 ID X HPBVI
 AC P20975;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw / strain Indonesia/PIDW420).
 OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10412;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89010694; PubMed=3171552;
 RA Okamoto H., Tsuda F., Sakugawa H., Sastroroenwignjo R.I., Imai M.,
 RA Miyakawa Y., Mayumi M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. Gen. Virol. 69:2575-2583(1988).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC
 DR EMBL; D00331; -, NOT_ANNOTATED_CDS.
 DR PIR; JS0604;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 SQ SEQUENCE 154 AA; 16556 MW; C80C817E961BFFB9 CRC64;

Query Match 76.4%; Score 42; DB 1; Length 154;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLFQWHEEL 9
 ||| |||||
 Db 115 CVTFWHEEL 123

RESULT 12

HEL5 PYRHO STANDARD; PRT; 715 AA.
 ID HEL5 PYRHO
 AC OS9025;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative sk12-type helicase (EC 3.6.1.-).
 GN PH1280.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;

RN SEQUENCE FROM N.A.
 RP STRAIN=OT3;
 RC MEDLINE=98344137; PubMed=9679194;
 RX Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo H. Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SK12 SUBFAMILY.

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 CC
 DR EMBL; AF000005; BAA30383.1; -.
 DR PIR; E71073; E71073.
 DR HAMAP; MF_00442; -; 1.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000445; HhH.
 DR InterPro; IPR003583; HHH_1.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; helicase_C; 1.
 DR Pfam; PF00633; HHH; 2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR SMART; SM00278; HHH1; 2.
 KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
 KW Complete proteome.

FT NP BIND 46 53 ATP (POTENTIAL).
 FT SITE 145 148 DEXH BOX.
 SQ SEQUENCE 715 AA; 82105 MW; F0E2A1AC765C999C CRC64;
 Query Match 76.4%; Score 42; DB 1; Length 715;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FQDWHEEL 9
 ||| |||||
 Db 86 FQDWHEEL 94

RESULT 13

DPOL_ADEB3 STANDARD; PRT; 1023 AA.
 ID DPOL_ADEB3
 AC O72540;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 GN POL.
 OS Bovine adenovirus type 3 (Mastadenovirus bos3).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WER-1;
 RX MEDLINE=99040086; PubMed=9820840;
 RA Yagubi A., Ojic D., Bautista D., Haj-Ahmad Y.;
 RT "Sequencing analysis of the region encoding the DNA polymerase of
 RT bovine adenovirus serotypes 2 and 3.";
 RL Intervirology 41:69-79(1998).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA} (N).

```

CC -1- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF061654; AAC16240.1; -
CC InterPro; IPR006172; DNA pol B.
CC Pfam; PF03175; DNA pol B_2; I.
CC SMART; SM00486; POLBc_1;
CC PROSITE; PS00116; DNA_POLYMERASE_B; 1.
CC Transferrase; DNA-directed DNA polymerase; DNA replication;
CC DNA-binding.
CC SEQUENCE 1023 AA; 117728 MW; 193998701764957A CRC64;
CC -----
Query Match 69.1%; Score 38; DB 1; Length 1023;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 FKDWEE 8
DB 294 FKDWEE 299
CC -----
RESULT 14
HEL5_PYPAB STANDARD; PRT; 715 AA.
ID HEL5_PYPAB
AC Q9V0A9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Purative ski2-type helicase (EC 3.6.1.1.-).
GN PYRAB08810 OR PAB0592.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GR5 / Orsay;
RX PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaean Pyrococcus abyssi."
RL Mol. Microbiol. 47:1495-1512(2003).
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
CC -----
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CC -----
CC EMBL; AJ248285; CAB49795.1; -
CC PIR; B75135; B75135.
CC HAMAP; MF 00442; 1.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR001650; Helicase_C.
CC InterPro; IPR000445; HHH.
CC Pfam; PF00270; DEAD_1.
CC Pfam; PF00271; helicase_C; 1.
CC Pfam; PF00633; HHH; 2.

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DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR SMART; SM00278; HHL1; 2.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
KW Complete proteome.
FT NF_BIND 46 53 ATP (POTENTIAL).
FT SITE 145 148 DEXH BOX.
SQ SEQUENCE 715 AA; 82005 MW; 611401E623690EF4 CRC64;
CC -----
Query Match 67.3%; Score 37; DB 1; Length 715;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 FKDWEE 9
DB 88 FKDWEE 94
CC -----
RESULT 15
YCF1_PINTH STANDARD; PRT; 1756 AA.
ID YCF1_PINTH
AC P41647;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 205.3 kDa protein ycf1 (ORF 1756).
GN YCF1.
OS Pinus thunbergii (Green pine) (Japanese black pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3350;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95024047; PubMed=7937893;
RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
RA Sugura M.;
RT "Loss of all ndh genes as determined by sequencing the entire
RT chloroplast genome of the black pine Pinus thunbergii."
RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
CC -1- FUNCTION: NOT YET KNOWN.
CC -1- SIMILARITY: BELONGS TO THE YCF1 FAMILY.
CC -----
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CC -----
CC EMBL; D17510; BAA04442.1; -
CC PIR; T07566; T07566.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 1756 AA; 205320 MW; 15C9946A8E8E7B56 CRC64;
CC -----
Query Match 67.3%; Score 37; DB 1; Length 1756;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 FKDWEE 9
DB 849 FKDWEE 855
CC -----
Search completed: December 23, 2003, 08:41:52
Job time : 8.4 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-4

Perfect score: 55

Sequence: 1 CLFKDWEEL 9

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mnc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	58	12	Q9E0S8 hepatitis b
2	55	100.0	58	12	Q9E0Q4 hepatitis b
3	55	100.0	58	12	Q9E0P6 hepatitis b
4	55	100.0	58	12	Q9E0U2 hepatitis b
5	55	100.0	58	12	Q9E0W2 hepatitis b
6	55	100.0	58	12	Q9E0S4 hepatitis b
7	55	100.0	58	12	Q9E0P2 hepatitis b
8	55	100.0	58	12	Q9E0S6 hepatitis b
9	55	100.0	58	12	Q9E0U0 hepatitis b
10	55	100.0	58	12	Q9E0Q2 hepatitis b
11	55	100.0	58	12	Q9E0N3 hepatitis b
12	55	100.0	58	12	Q9E0S2 hepatitis b
13	55	100.0	58	12	Q9E0W6 hepatitis b
14	55	100.0	58	12	Q9E0R4 hepatitis b
15	55	100.0	58	12	Q9E0W8 hepatitis b
16	55	100.0	58	12	Q9E0T4 hepatitis b

17	55	100.0	58	12	Q9E0P0	Q9E0P0 hepatitis b
18	55	100.0	58	12	Q9E0V2	Q9E0V2 hepatitis b
19	55	100.0	58	12	Q9E0U8	Q9E0U8 hepatitis b
20	55	100.0	58	12	Q9E0V4	Q9E0V4 hepatitis b
21	55	100.0	58	12	Q9E0W0	Q9E0W0 hepatitis b
22	55	100.0	58	12	Q9E0U4	Q9E0U4 hepatitis b
23	55	100.0	58	12	Q9E0T0	Q9E0T0 hepatitis b
24	55	100.0	58	12	Q9E0N6	Q9E0N6 hepatitis b
25	55	100.0	58	12	Q9E0V6	Q9E0V6 hepatitis b
26	55	100.0	58	12	Q9E0P4	Q9E0P4 hepatitis b
27	55	100.0	58	12	Q9E0T2	Q9E0T2 hepatitis b
28	55	100.0	58	12	Q9E0R8	Q9E0R8 hepatitis b
29	55	100.0	58	12	Q9E0P8	Q9E0P8 hepatitis b
30	55	100.0	58	12	Q9E0R0	Q9E0R0 hepatitis b
31	55	100.0	58	12	Q9E0R2	Q9E0R2 hepatitis b
32	55	100.0	58	12	Q9E0V0	Q9E0V0 hepatitis b
33	55	100.0	58	12	Q9E0Q8	Q9E0Q8 hepatitis b
34	55	100.0	58	12	Q9E0T6	Q9E0T6 hepatitis b
35	55	100.0	58	12	Q9E0N8	Q9E0N8 hepatitis b
36	55	100.0	58	12	Q9E0U6	Q9E0U6 hepatitis b
37	55	100.0	58	12	Q9E0Q0	Q9E0Q0 hepatitis b
38	55	100.0	58	12	Q9E0Q6	Q9E0Q6 hepatitis b
39	55	100.0	58	12	Q9E0W4	Q9E0W4 hepatitis b
40	55	100.0	58	12	Q9E0S0	Q9E0S0 hepatitis b
41	55	100.0	58	12	Q9E0V8	Q9E0V8 hepatitis b
42	55	100.0	130	12	Q91SG7	Q91SG7 hepatitis b
43	55	100.0	130	12	Q9DKT3	Q9DKT3 hepatitis b
44	55	100.0	134	12	Q91SG6	Q91SG6 hepatitis b
45	55	100.0	134	12	Q90073	Q90073 hepatitis b

ALIGNMENTS

RESULT 1

Q9E0S8 PRELIMINARY; PRT; 58 AA.
ID Q9E0S8
AC Q9E0S8 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE X protein (Fragment).
GN X
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSsCO36;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289954; AAG25247.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6520 MW; 39D3CAC56C6BE20 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

|||||

19 CLFKDWEEL 27

RESULT 2

Q9E0Q4 PRELIMINARY; PRT; 58 AA.

ID Q9E0Q4

AC Q9E0Q4;

```

DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=BBSC0324;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289966; AAG25271.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6473 MW; 4ED3CAC135124BE2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 3
Q9EOP6 PRELIMINARY; PRT; 58 AA.
AC Q9EOP6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=BBSC0412;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289970; AAG25279.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6464 MW; 195CACDA94A848F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 4
Q9EQU2 PRELIMINARY; PRT; 58 AA.
AC Q9EQU2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.

```

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DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=BBSC0115;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289947; AAG25233.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 5
Q9EOW2 PRELIMINARY; PRT; 58 AA.
AC Q9EOW2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=BBSC058;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289937; AAG25213.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER 1
SQ SEQUENCE 58 AA; 6506 MW; 6E5CACDDFDE2FE36 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWHEEL 9
DB 19 CLFKDWHEEL 27

RESULT 6
Q9EOS4 PRELIMINARY; PRT; 58 AA.
AC Q9EOS4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.

```

OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0138;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289956; AAG25251.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADD84DF48E2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 DB 19 CLFKDWEEL 27

RESULT 7

Q9E0P2
 ID Q9E0P2 PRELIMINARY; PRT; 58 AA.
 AC Q9E0P2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0380;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289972; AAG25283.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6490 MW; 195CACC1351248F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 DB 19 CLFKDWEEL 27

RESULT 8

Q9E0S6
 ID Q9E0S6 PRELIMINARY; PRT; 58 AA.
 AC Q9E0S6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0152;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289955; AAG25249.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6487 MW; 485DACC1351248E8 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 DB 19 CLFKDWEEL 27

RESULT 9

Q9E0U0
 ID Q9E0U0 PRELIMINARY; PRT; 58 AA.
 AC Q9E0U0;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0148;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;
 RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
 RT HBV Isolated from Patients with Hepatocellular Carcinoma and
 RT Controls";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289948; AAG25235.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 SQ SEQUENCE 58 AA; 6487 MW; 049D70C1351248F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 DB 19 CLFKDWEEL 27

RESULT 10

Q9EQ02
 ID Q9EQ02 PRELIMINARY; PRT; 58 AA.
 AC Q9EQ02;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE x protein (Fragment).
 GN X.
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BBSC0354;
 RA Tagger A., Binelli G., Donato F., Ribero M.L.;

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RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289967; AAG25273.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 58 AA; 6461 MW; 4ED3CADDE4DF48E2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
DB 19 CLFKDWEEL 27

RESULT 11
Q9EON3 PRELIMINARY; PRT; 58 AA.
AC Q9EON3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSC396;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289977; AAG25292.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 58 AA; 6508 MW; ECSCACDDF6F48EE CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
DB 19 CLFKDWEEL 27

RESULT 12
Q9E0S2 PRELIMINARY; PRT; 58 AA.
AC Q9E0S2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSHCC308;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289957; AAG25253.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 58 AA; 6494 MW; B8B3BDDDE4DF48FF CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
DB 19 CLFKDWEEL 27

RESULT 13
Q9E0W6 PRELIMINARY; PRT; 58 AA.
AC Q9E0W6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBHCC53;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289935; AAG25209.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON TER
SQ SEQUENCE 58 AA; 6464 MW; 195CACDA94A848F4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
DB 19 CLFKDWEEL 27

RESULT 14
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AC Q9E0R4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBSHCC259;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289961; AAG25261.1; -.
DR InterPro; IPR000236; TransactX.

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DR Pfam: PF00739; X; 1.
FT NON_TER 1 1
SQ SEQUENCE 58 AA; 6478 MW; 195CACDDE4DF48F4 CRC64;

Query Match      100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLPKDWHEEL 9
Db 19 CLPKDWHEEL 27

RESULT 15
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AC Q9ECW8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BBsHCC24;
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RT "Prevalence of 1762T and 1764A Mutations in the Basic Core Promoter of
RT HBV Isolated from Patients with Hepatocellular Carcinoma and
RT Controls.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289334; AAC25208.1; --
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
SQ SEQUENCE 58 AA; 6537 MW; 7ESDACDDFDE2FE36 CRC64;

Query Match      100.0%; Score 55; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLPKDWHEEL 9
Db 19 CLPKDWHEEL 27

Search completed: December 23, 2003, 08:46:11
Job time : 24.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:40:03 ; Search time 79.4 Seconds
(without alignments)
21.169 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41
Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	41	100.0	9	10	US-09-989-621-5
2	37	90.2	154	15	US-10-209-264-5
3	34	82.9	201	15	US-10-013-315-36
4	34	82.9	476	8	US-08-834-705-4
5	31	75.6	230	12	US-10-084-843-65
6	31	75.6	230	12	US-10-193-002-66
7	30	73.2	85	10	US-09-987-108-28
8	30	73.2	589	12	US-10-205-194-144
9	29	70.7	68	11	US-09-764-891-3030
10	29	70.7	344	9	US-09-741-669-308
11	29	70.7	344	9	US-09-912-020-285
12	28	68.3	57	9	US-09-864-761-37657
13	28	68.3	87	14	US-10-001-876-118
14	28	68.3	98	10	US-09-881-752A-182
15	28	68.3	156	15	US-10-074-475-237

16	28	68.3	233	14	US-10-138-787-7	Sequence 7, Appli
17	28	68.3	238	9	US-09-904-954-2	Sequence 72, Appli
18	28	68.3	238	12	US-10-241-220-72	Sequence 2, Appli
19	28	68.3	238	12	US-09-733-756-2	Sequence 2, Appli
20	28	68.3	253	12	US-10-017-161-626	Sequence 626, App
21	28	68.3	279	9	US-09-846-808-21	Sequence 21, Appli
22	28	68.3	279	12	US-10-369-293-21	Sequence 21, Appli
23	28	68.3	279	12	US-10-285-042-21	Sequence 21, Appli
24	28	68.3	279	15	US-10-284-986-21	Sequence 21, Appli
25	28	68.3	311	10	US-09-886-055-59	Sequence 59, Appli
26	28	68.3	311	11	US-09-804-291-59	Sequence 59, Appli
27	28	68.3	311	12	US-10-387-629-82	Sequence 82, Appli
28	28	68.3	313	10	US-09-886-055-169	Sequence 169, App
29	28	68.3	313	11	US-09-804-291-169	Sequence 169, App
30	28	68.3	313	12	US-10-017-161-250	Sequence 250, App
31	28	68.3	386	12	US-10-177-478-4	Sequence 13, Appli
32	28	68.3	386	15	US-10-176-884-13	Sequence 2190, Ap
33	28	68.3	401	12	US-10-094-749-2190	Sequence 46, Appli
34	28	68.3	1152	11	US-09-374-046A-46	Sequence 12, Appli
35	27	65.9	155	14	US-10-001-835-213	Sequence 205, App
36	27	65.9	205	12	US-10-099-323-12	Sequence 6, Appli
37	27	65.9	209	9	US-09-811-284-205	Sequence 9, Appli
38	27	65.9	209	10	US-09-921-984-2	Sequence 295, App
39	27	65.9	209	14	US-10-138-787-6	Sequence 381, App
40	27	65.9	228	8	US-08-578-684-4	Sequence 406, App
41	27	65.9	228	14	US-10-138-787-9	
42	27	65.9	231	9	US-09-912-020-295	
43	27	65.9	307	10	US-09-886-055-381	
44	27	65.9	307	11	US-09-804-291-381	
45	27	65.9	307	12	US-10-017-161-406	

ALIGNMENTS

RESULT 1
US-09-989-621-5
; Sequence 5, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Wyeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-989-621-5

Query Match 100.0%; Score 41; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKVFL 9
Db 1 EIRLKVFL 9

RESULT 2

US-10-209-264-5
; Sequence 5, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oor, Chong Jin
; Lim, Gek Keow
; Zhao, Yi
; Chen, Wei Ning
; TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/209,264
; FILING DATE: 31-Jul-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SG98/00046
; FILING DATE: 19-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-013109-7
; TELEPHONE: (212) 708-1800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-209-264-5
Query Match 90.2%; Score 37; DB 15; Length 154;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IRLKVFVL 9
Db 126 IRLKIIVL 134
RESULT 3
US-10-013-315-36
; Sequence 36, Application US/10013315
; Publication No. US20030069404A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Rainer
; APPLICANT: Kleanthous, Harold
; APPLICANT: Meyer, Thomas F.
; APPLICANT: Odenbreit, Stefan
; APPLICANT: Al-Garawi, Amal A.
; APPLICANT: Miller, Charles A.
; TITLE OF INVENTION: New Helicobacter Antigens and
; USES THEREOF
; FILE REFERENCE: 06132/028002
; CURRENT APPLICATION NUMBER: US/10/013,315
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 08/749,051
; FILING DATE: 1996-11-14
; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-013-315-36
Query Match 82.9%; Score 34; DB 15; Length 201;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 IRLKVFVL 9
Db 6 VRLKIFVL 13
RESULT 4
US-08-834-705-4
; Sequence 4, Application US/08834705
; Publication No. US20030023066A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Rainer et al.
; TITLE OF INVENTION: New Helicobacter Polypeptides
; AND CORRESPONDING Polynucleotide Molecules
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Ribing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,705
; FILING DATE: 01-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/749,051
; FILING DATE: 14-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,175
; REFERENCE/DOCKET NUMBER: 06132/039001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...25
; OTHER INFORMATION:
US-08-834-705-4
Query Match 82.9%; Score 34; DB 8; Length 476;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 IRLKVFVL 9
Db 6 VRLKIFVL 13

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RESULT 5
US-10-084-843-65
; Sequence 65, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
;           Skeiky, Yasir A.W.
;           Dillon, Davin C.
;           Campos-Neto, Antonio
;           Houghton, Raymond
;           Vedvick, Thomas S.
;           Twardzik, Daniel R.
;           Lodes, Michael J.
;           Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;                   AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,843
; FILING DATE: 25-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-084-843-65
; Query Match 75.6%; Score 31; DB 12; Length 230;
; Best Local Similarity 44.4%; Pred. No. 79;
; Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BIRLKVFL 9
Db 66 DVRKIFML 74

RESULT 6
US-10-193-002-66
; Sequence 66, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
;           Skeiky, Yasir A.W.
;           Dillon, Davin C.
;           Campos-Neto, Antonio
;           Houghton, Raymond

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;           Vedvick, Thomas S.
;           Twardzik, Daniel R.
;           Lodes, Michael J.
;           Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
;                   TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/193,002
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-193-002-66
; Query Match 75.6%; Score 31; DB 12; Length 230;
; Best Local Similarity 44.4%; Pred. No. 79;
; Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BIRLKVFL 9
Db 66 DVRKIFML 74

RESULT 7
US-09-987-108-28
; Sequence 28, Application US/09987108
; Patent No. US20020142347A1
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, Jens
; APPLICANT: WADUM, Maiken C.T.
; APPLICANT: VILLADSEN, Jens
; APPLICANT: NEERGAARD, Thomas B.F.
; TITLE OF INVENTION: BIOSENSOR
; FILE REFERENCE: KNUDSENIA
; CURRENT APPLICATION NUMBER: US/09/987,108
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/262,366
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: DK PA2000 01638
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 85
; TYPE: PRI

```

! ORGANISM: Cyprinus carpio
US-09-987-108-28

Query Match 73.2%; Score 30; DB 10; Length 85;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 22 EVLKVVAL 30

RESULT 8
US-10-205-194-144
! Sequence 144, Application US/10205194
! Publication No. US2003013430A1
! GENERAL INFORMATION:
! APPLICANT: Warner-Lambert Company
! APPLICANT: Lee, Kevin
! APPLICANT: Dixon, Alistair
! APPLICANT: Brooksbank, Robert
! APPLICANT: Pinnock, Robert
! TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
! FILE REFERENCE: WL-A-018201
! CURRENT APPLICATION NUMBER: US/10/205,194
! CURRENT FILING DATE: 5200-07-24
! PRIOR FILING DATE: 2001-07-27
! PRIOR APPLICATION NUMBER: GB 0118354.0
! NUMBER OF SEQ ID NOS: 177
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 144
! LENGTH: 589
! TYPE: PRT
! ORGANISM: Mus musculus
! FEATURE:
! OTHER INFORMATION: Rnal homolog
US-10-205-194-144

Query Match 73.2%; Score 30; DB 12; Length 589;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IRLKVFV 8
DB 180 ELRLKVFV 186

RESULT 9
US-09-764-891-3030
! Sequence 3030, Application US/09764891
! Publication No. US20030077808A1
! GENERAL INFORMATION:
! APPLICANT: Rosen et al.
! TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
! FILE REFERENCE: PC006
! CURRENT APPLICATION NUMBER: US/09/764,891
! CURRENT FILING DATE: 2001-01-17
! Prior application data removed - consult PAM or file wrapper
! NUMBER OF SEQ ID NOS: 10231
! SOFTWARE: PatentIn Ver. 2.0
! SEQ ID NO 3030
! LENGTH: 68
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-764-891-3030

Query Match 70.7%; Score 29; DB 11; Length 68;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 54 ELRVKDFVL 62

RESULT 10
US-09-741-669-308
! Sequence 308, Application US/09741669
! Patent No. US2002002718A1
! GENERAL INFORMATION:
! APPLICANT: Forsyth, R. Allyn
! APPLICANT: Ohlsen, Kari L.
! APPLICANT: Zyskind, Judith W.
! TITLE OF INVENTION: Genes identified as required for
! proliferation of E. coli
! FILE REFERENCE: ELITRA.009A
! CURRENT APPLICATION NUMBER: US/09/741,669
! CURRENT FILING DATE: 2000-12-19
! PRIOR FILING DATE: 1999-12-23
! PRIOR APPLICATION NUMBER: US 60/173005
! NUMBER OF SEQ ID NOS: 481
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 308
! LENGTH: 344
! TYPE: PRT
! ORGANISM: Escherichia coli
US-09-741-669-308

Query Match 70.7%; Score 29; DB 9; Length 344;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 2 EIRIMLFL 10

RESULT 11
US-09-912-020-285
! Sequence 285, Application US/09912020
! Patent No. US20020045592A1
! GENERAL INFORMATION:
! APPLICANT: Zyskind, Judith
! APPLICANT: Ohlsen, Kari L.
! APPLICANT: Trawick, John
! APPLICANT: Forsyth, R. Allyn
! APPLICANT: Froelich, Jamie M.
! APPLICANT: Carr, Grant J.
! APPLICANT: Yamamoto, Robert T.
! APPLICANT: Xu, H. Howard
! TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
! FILE REFERENCE: ELITRA.001DV1
! CURRENT APPLICATION NUMBER: US/09/912,020
! CURRENT FILING DATE: 2001-07-23
! PRIOR APPLICATION NUMBER: 09/492,709
! PRIOR FILING DATE: 2000-01-27
! PRIOR APPLICATION NUMBER: 60/117,405
! NUMBER OF SEQ ID NOS: 485
! SOFTWARE: FastSeq for Windows Version 3.0
! SEQ ID NO 285
! LENGTH: 344
! TYPE: PRT
! ORGANISM: E. Coli
US-09-912-020-285

Query Match 70.7%; Score 29; DB 9; Length 344;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 2 EIRIMLFL 10

RESULT 12

US-09-864-761-37657
; Sequence 37657, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aescica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37657
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010491.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EST HUMAN HIT: AAL33798.1, EVALUATE 1.00e-22
; OTHER INFORMATION: SWISSPROT HIT: O00321, EVALUATE 5.80e+00
; US-09-864-761-37657

Query Match

68.3%; Score 28; DB 9; Length 57;

Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;QY 1 EIRLKVFVL 9
|:::|
DB 11 EVKIKVFL 19

RESULT 13

US-10-001-876-118
; Sequence 118, Application US/10001876
; Publication No. US20020177140A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0285
; CURRENT APPLICATION NUMBER: US/10/001,876
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,186
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-001-876-118

Query Match 68.3%; Score 28; DB 14; Length 87;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;QY 1 EIRLKVF 7
|:::|
DB 67 EMRMKVF 73

RESULT 14

US-09-881-752A-182
; Sequence 182, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleathous, Harold
; APPLICANT: Al-Gatawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Comen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; FILE REFERENCE: Encoding No. US20020115078A1el Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-09-881-752A-182

Query Match 68.3%; Score 28; DB 10; Length 98;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLKVFL 9
|:|:|:|
Db 64 EIKIEAFVL 72

RESULT 15

US-10-074-475-237
; Sequence 237, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Kaxra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; FILE REFERENCE: DEX-0313
; CURRENT APPLICATION NUMBER: US/10/074,475
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,292
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-074-475-237

Query Match 68.3%; Score 28; DB 15; Length 156;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IRLKVFL 8
|:|:|:|
Db 34 VRMKVFI 40

Search completed: December 23, 2003, 08:52:50
Job time : 79.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 11 Seconds
(without alignments)
78.683 Million cell updates/sec

Title: US-09-989-621-5

Perfect score: 41

Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PR: 76:*

1: pr1:*

2: pr2:*

3: pr3:*

4: pr4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	31	2 S53187	gene X protein - h
2	41	100.0	31	2 S53190	gene X protein - h
3	41	100.0	31	2 S53199	gene X protein - h
4	41	100.0	31	2 S53254	gene X protein - h
5	41	100.0	31	2 S53282	gene X protein - h
6	41	100.0	154	1 QVLD1	gene X protein - h
7	41	100.0	154	1 QVLDH	gene X protein - h
8	41	100.0	154	1 A48345	gene X protein - h
9	41	100.0	154	1 QVLDW	gene X protein - h
10	41	100.0	154	1 QVLDK	gene X protein - h
11	41	100.0	154	1 QVLDK	gene X protein - h
12	41	100.0	154	1 QVLDK	gene X protein - h
13	41	100.0	154	2 J50256	gene X protein - h
14	41	100.0	154	2 J50256	trans-activating p
15	41	100.0	154	2 J50256	gene X protein - h
16	41	100.0	154	2 J50604	gene X protein - h
17	41	100.0	154	2 S35529	gene X protein - h
18	41	100.0	154	2 S33687	gene X protein - h
19	41	100.0	154	2 S12542	gene X protein - h
20	41	100.0	154	2 S32203	gene X protein - h
21	41	100.0	154	2 S20751	gene X protein - h
22	40	97.6	31	2 S53132	gene X protein - h
23	40	97.6	31	2 S53138	gene X protein - h
24	40	97.6	31	2 S53233	gene X protein - h
25	40	97.6	31	2 S53287	gene X protein - h
26	40	97.6	154	2 S47404	gene X protein - h
27	40	97.6	154	2 J50603	gene X protein - h
28	39	95.1	31	2 S53156	gene X protein - h
29	38	92.7	31	2 S53162	gene X protein - h

ALIGNMENTS

RESULT 1

S53187
gene X protein - hepatitis B virus (isolate patient Serra'89) (fragment)
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Serra'89
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53187
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53187
A:Molecule type: DNA
A:Residues: 1-31 <LAI>
A:Cross-references: EMBL:X85282; NID:g736084; PIDN:CAA59592.1; PID:g736085
A:Experimental source: isolate patient Serra'89
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

DB 3 EIRLKVFL 11

RESULT 2

S53190
gene X protein - hepatitis B virus (isolate patient Ferracuti'83) (fragment)
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Ferracuti'83
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53190
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53190
A:Molecule type: DNA
A:Residues: 1-31 <LAI>
A:Cross-references: EMBL:X85283; NID:g736088; PIDN:CAA59592.1; PID:g736089
A:Experimental source: isolate patient Ferracuti'83
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

gene X protein - hepatitis B virus (isolate patient Galistru'85) (fragment)
 Species: hepatitis B virus, HBV
 Variety: isolate patient Galistru'85
 Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 Accession: S53282
 Author: Lai, M.E.; Mazzoleni, A.P.; Portu, A.; Balesrieri, A.
 Submitted to the EMBL Data Library, March 1995
 Reference number: S53112
 Accession: S53282
 Molecule type: DNA
 Residues: 1-31 <LAI>

EMBL/Accession: 124-134 <LA2>
A/Cross-references: EMBL:X85277; NID:q736065; PIDN:CAA59575.1; PID:q736066

A;/Experimental source: isolate patient Bio'90

C;/Genetics:

A;/Gene: X

C;/Superfamily: hepatitis B virus gene X protein

Query Match 100.0%; Score 41; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

1111111111

Db 126 EIRLKVFL 134

RESULT 8

A48345

gene X protein - hepatitis B virus

C;/Species: hepatitis B virus, HBV

C;/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C;/Accession: A48345

R;/Repp, R.; Keller, C.; Borkhardt, A.; Csecke, A.; Schaefer, S.; Gerlich, W.H.; Lampert,

Arch. Virol. 125, 299-304, 1992

A;/Title: Detection of a hepatitis B virus variant with a truncated X gene and enhancer

A;/Reference number: A48345; MUID:92352333; PMID:1642555

A;/Accession: A48345

A;/Molecule type: DNA

A;/Residues: 1-154 <REP>

A;/Cross-references: GB:S41175; NID:9252539; PIDN:AAB22732.1; PID:9252540

A;/Note: sequence extracted from NCBI backbone (NCBI:109912, NCBI:109913)

C;/Genetics:

A;/Gene: X

C;/Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

1111111111

Db 126 EIRLKVFL 134

RESULT 9

QOVLAW

gene X protein - hepatitis B virus (subtype adw and adw2)

C;/Species: hepatitis B virus, HBV

C;/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 30-Jun-1998

C;/Accession: A31289; B94409; A03719

R;/Lo, S.J.; Chien, W.L.; Lee, Y.H.W.

Virol. 167, 289-292, 1989

A;/Title: Characteristics of the X gene of hepatitis B virus.

A;/Reference number: A31289; MUID:89045656; PMID:3188399

A;/Accession: A31289

A;/Molecule type: DNA

A;/Residues: 1-154 <LOS>

A;/Experimental source: subtype adw

R;/Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.

in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Acad

A;/Reference number: A94409

A;/Accession: B94409

A;/Molecule type: DNA

A;/Residues: 1-154 <VAL>

A;/Experimental source: subtype adw2

C;/Genetics:

A;/Gene: X

C;/Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

1111111111

Db 126 EIRLKVFL 134

RESULT 10

QOVLKS

gene X protein - hepatitis B virus (subtype adw, strain 991)

C;/Species: hepatitis B virus, HBV

C;/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C;/Accession: S10380

R;/Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomssen, R.

submitted to the EMBL Data Library, February 1990

A;/Reference number: S10380

A;/Accession: S10380

A;/Molecule type: DNA

A;/Residues: 1-154 <KOE>

A;/Cross-references: EMBL:X51970; NID:gi155012; PIDN:CAA36231.1; PID:g60432

C;/Genetics:

A;/Gene: X

C;/Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

1111111111

Db 126 EIRLKVFL 134

RESULT 11

QOVLCP

gene X protein - hepatitis B virus (strain LSH, chimpanzee)

C;/Species: hepatitis B virus, HBV

C;/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000

C;/Accession: D28885

R;/Vaundon, M.; Wolstenholme, A.J.; Tsiuaye, K.N.; Zuckerman, A.J.; Harrison, T.J.

J. Gen. Virol. 69, 1383-1389, 1988

A;/Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated

A;/Reference number: A92796; MUID:88258473; PMID:2838576

A;/Accession: D28885

A;/Molecule type: DNA

A;/Residues: 1-154 <VAU>

A;/Cross-references: GB:D00220; NID:g221505; PIDN:BAA00160.1; PID:g221509

C;/Genetics:

A;/Gene: X

C;/Superfamily: hepatitis B virus gene X protein

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 154;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

1111111111

Db 126 EIRLKVFL 134

RESULT 12

S20756

gene X protein - hepatitis B virus (subtype ayw, patient B)

C;/Species: hepatitis B virus, HBV

A;/Variety: subtype ayw, patient B

C;/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;/Accession: S20756

R;/Jai, M.E.; Mazoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.

submitted to the EMBL Data Library, March 1992

A;/Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati

A;/Reference number: S20745

A;/Accession: S20756

A;/Molecule type: DNA

A;/Residues: 1-154 <LAI>

A;/Cross-references: EMBL:X65259; NID:g59439; PIDN:CAA46360.1; PID:g59443

A;/Experimental source: subtype ayw, patient E

C;/Genetics:

```

A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 13
JS0256
gene X protein - hepatitis B virus (subtype adv, strain Japan/pJ2W233)
C:Species: hepatitis B virus, HBV
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 14-Nov-1997
C:Accession: JS0256
R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrocewignjo, R.I.; Imai, M.; Miyakawa, Y.;
J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur
A:Reference number: JS0253; MUID:89010694; PMID:3171552
A:Accession: JS0256
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <OKA>
A:Cross-references: GB:D00329; NID:G221497
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 14
JQ2228
trans-activating protein X - hepatitis B virus
N:Alternate names: HBx protein
C:Species: hepatitis B virus, HBV
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 26-Aug-1999
C:Accession: JQ2228; S31794
R:Naumann, H.; Schaefer, S.; Yoshida, C.F.T.; Gaspar, A.M.C.; Repp, R.; Gerlich, W.H.
J. Gen. Virol. 74, 1627-1632, 1993
A:Title: Identification of a new hepatitis B virus (HBV) genotype from Brazil that expre
A:Reference number: JQ2225; MUID:93346970; PMID:8345355
A:Accession: JQ2228
A:Molecule type: DNA
A:Residues: 1-154 <NAU>
A:Cross-references: EMBL:X69798; NID:G59422; PIDN:CAA49453.1; PID:G59424
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 15
S25650
gene X protein - hepatitis B virus (subtype ayw, patient D)
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient D
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S25650

```

```

R:Lai, M.E.; Mazzoleni, A.P.; Melis, A.; Balestrieri, A.
submitted to the EMBL Data Library, September 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negat
A:Reference number: S25650
A:Accession: S25650
A:Molecule type: DNA
A:Residues: 1-154 <LAI>
A:Cross-references: EMBL:X68292; NID:G59448; PIDN:CAA48352.1; PID:G59449
A:Experimental source: subtype ayw, patient D
C:Genetics:
A:Gene: X
C:Superfamily: hepatitis B virus gene X protein

Query Match      100.0%; Score 41; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

Search completed: December 23, 2003, 08:41:09
Job time : 11 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 seconds
(without alignments)
66.131 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41
Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	154	1 X_HPBV2	P03166 hepatitis b
2	41	100.0	154	1 X_HPBV4	P12936 hepatitis b
3	41	100.0	154	1 X_HPBV9	P17102 hepatitis b
4	41	100.0	154	1 X_HPBV1	P20975 hepatitis b
5	41	100.0	154	1 X_HPBV7	P20976 hepatitis b
6	41	100.0	154	1 X_HPBV1	P12912 hepatitis b
7	41	100.0	154	1 X_HPBV1	Q05493 hepatitis b
8	41	100.0	154	1 X_HPBV1	P03165 hepatitis b
9	40	97.6	154	1 X_HPBV0	P20977 hepatitis b
10	34	82.9	154	1 X_HPBV4	P24026 hepatitis b
11	33	80.5	179	1 NUGC_SINY3	P31253 synchocyst
12	31	75.6	175	1 NUGC_ANASP	Q4241 anabaena sp
13	31	75.6	175	1 NUGC_ANAVA	Q9xb16 anabaena va
14	31	75.6	267	1 Y123 THEMA	Q9wx77 thermotoga
15	30	73.2	100	1 VE7_HPV38	Q80908 human papil
16	30	73.2	102	1 VE7_HPV36	P50811 human papil
17	30	73.2	223	1 RPE_ECOLI	P12972 escherichia
18	30	73.2	230	1 RPE_VIBCH	Q9k011 vibrio chol
19	30	73.2	589	1 RGP1_MOUSE	P46061 mus musculus
20	29	70.7	102	1 VE7_HPV25	P36823 human papil
21	29	70.7	103	1 VE7_HPV05	P06932 human papil
22	29	70.7	103	1 VE7_HPV47	P22423 human papil
23	29	70.7	103	1 VE7_HPV49	P36830 human papil
24	29	70.7	103	1 VE7_HPV5B	P26559 human papil
25	29	70.7	138	1 X_HBGS	P03148 ground squi
26	29	70.7	169	1 NUGC_MARPO	P33340 marchantia
27	29	70.7	344	1 YHAH_ECOLI	P33340 escherichia
28	29	70.7	373	1 ADHA_RABIT	O19053 coryctolagus
29	29	70.7	430	1 MTS9_STAAR	P23737 staphylococ
30	29	70.7	564	1 ATKA_PSEAE	P57683 pseudomonas
31	29	70.7	926	1 CTF4_YEAST	Q01454 saccharomyc
32	28	68.3	187	1 RPA3_MOUSE	Q08545 mus musculu
33	28	68.3	199	1 YD66_YEAST	P38962 saccharomyc

ALIGNMENTS

RESULT 1

ID	X_HPBV2	STANDARD;	PRT;	154 AA.
AC	P03166; P12935;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, last sequence update)			
DT	15-DEC-1998 (Rel. 37, last annotation update)			
DE	Trans-activating protein X.			
GN	X.			
OS	Hepatitis B virus (subtype adw2), and			
OS	Hepatitis B virus (subtype adw).			
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
OX	NCBI_TaxID=10408, 106821;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ADW2;			
RA	Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;			
RL	(In) Field B.N., Jaenisch R., Fox C.F. (eds.);			
RL	Animal Virus Genetics, pp.57-70, Academic Press, New York (1980).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ADW;			
RX	MEDLINE=89045656; PubMed=3188399;			
RA	Lo S.J., Chien M.L., Lee Y.H.W.;			
RL	"Characteristics of the X gene of hepatitis B virus.;"			
RL	Virology 167:289-292(1988).			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ADW;			
RX	MEDLINE=83168919; PubMed=6300776;			
RA	Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;			
RL	"The complete nucleotide sequences of the cloned hepatitis B virus			
RT	DNA; subtype adr and adw.;"			
RL	Nucleic Acids Res. 11:1747-1757(1983).			
CC	-!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.			
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CC	-----			
CC	EMBL; X02763; CAA26540.1; -			
DR	EMBL; Z35717; CAA84789.1; -			
DR	EMBL; M23592; AAA56820.1; -			
DR	EMBL; V00866; -; NOT_ANNOTATED_CDS.			
DR	PIR; A31289; QOVLAW.			
DR	PIR; S47408; S47408.			
DR	InterPro; IPR000236; TransactX.			
DR	Pfam; PF00739; X; 1.			
FT	CONFLICT 80 80 E -> A (IN REF. 3).			
FT	CONFLICT 115 115 C -> S (IN REF. 2).			
FT	CONFLICT 130 131 KV -> MI (IN REF. 3).			
FT	SEQUENCE 154 AA; 16583 MW; 7F2AE332A4F025670 CRC64;			

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Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 2
X HPBV4
ID X HPBV4 STANDARD; PRT; 154 AA.
AC PI2936;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyachara A., Nozaki C., Yoneyama T., Ontomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr";
RL Nucleic Acids Res. 11:4601-4610(1983).
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CC
CC EMBL; X01587; CAA25744.1;
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 3
X HPBV9
ID X HPBV9 STANDARD; PRT; 154 AA.
AC PI7102;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; X51970; CAA36231.1;
CC PIR; S10380; QOVLKS.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16553 MW; 52A0D9CEFB6DCDE0 CRC64;

Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 4
X HPBV1
ID X HPBV1 STANDARD; PRT; 154 AA.
AC P20975;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Indonesia/p1dW420).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastroroenigjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC
CC EMBL; D00331; NOT_ANNOTATED_CDS.
CC PIR; JS0604; JS0604.
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
CC SEQUENCE 154 AA; 16556 MW; C80C817E961BFFB9 CRC64;

Query Match      100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
Db 126 EIRLKVFL 134

RESULT 5
X HPBVU
ID X HPBVU STANDARD; PRT; 154 AA.
AC P20976;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Japan/PJRW233).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Teuda F., Sakugawa H., Sastrosowignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
DR EMBL; D00329; ; NOT_ANNOTATED_CDS.
DR PIR; J50256; JS0256;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
DR SEQUENCE 154 AA; 16595 MW; 512A5A077169D5CA CRC64;
SQ
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 6
X_HPBVL STANDARD; PRT; 154 AA.
AC
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC -----
DR EMBL; D00220; BAA00160.1; -
DR PIR; D28885; QOVLCP.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 7
X_HPBVL STANDARD; PRT; 154 AA.
AC
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1627-1632(1993).
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CC -----
DR EMBL; X59798; GAA49453.1; -
DR PIR; JQ2228; JQ2228.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
DR SEQUENCE 154 AA; 16715 MW; E523C051B9B0B737 CRC64;
SQ
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 8
X_HPBVL STANDARD; PRT; 154 AA.
AC
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Pitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)

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RT cloned in E. coli.";
RN Nature 281:646-650(1979).
RP [2].
RC SEQUENCE FROM N.A.
RA STRAIN=Latvia;
RX MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
analysis";
RL FEBS Lett. 185:208-212(1985).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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CC
CC EMBL; V01460; -; NOT ANNOTATED_CDS.
DR EMBL; X02496; CAB41657.1; -;
DR PIR; A03719; QOVLDI.
DR PIR; A05237; QOVLH.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT VARIANT 46 46
FT VARIAT 84 88 P -> S (IN STRAIN LATVIA).
FT VARIAT 102 102 A -> V (IN STRAIN LATVIA).
FT CONFLICT 26 26 R -> C (IN REF. 1).
FT SEQUENCE 154 AA; 16618 MW; 29FD1CC9E09A34B5 CRC64;
SQ
Query Match 100.0%; Score 41; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 9
X HPBVA STANDARD; PRT; 154 AA.
AC P20977;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Okinawa/PODW282).
OC Viruses; Retroviridae; Orthohepadnavirus.
OX NCBI_taxid=10415;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosaswignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; D00330; -; NOT ANNOTATED_CDS.
DR EMBL; J06063; J0603.
DR PIR; J06063; J0603.

```

```

DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;
Query Match 97.6%; Score 40; DB 1; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 10
X HPBVA STANDARD; PRT; 154 AA.
AC P24026;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retroviridae; Orthohepadnavirus.
OX NCBI_taxid=10411;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Treppe C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; M32138; AAA45504.1; -;
DR EMBL; D34773; QOVLAI.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16671 MW; 2CFEEA77FA5E271F CRC64;
Query Match 82.9%; Score 34; DB 1; Length 154;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134
RESULT 11
NUGC SYN3 STANDARD; PRT; 179 AA.
AC P19125; P74194.
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-guanylate cyclase subunit J (EC 1.6.5.-) (NAD(P)H
DE dehydrogenase I, subunit J) (NDH-1, subunit J) (ORF 155).
GN NDHJ OR SLR1281.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_taxid=1149;
RN [1]
SEQUENCE FROM N.A.
RP SEQUENCE=89281491; PubMed=2499764;
RX MEDLINE=89281491; PubMed=2499764;

```

Steinmueller K., Ley A.C., Steinmetz A.A., Sayre R.T., Bogorad L.;
"characterization of the ndhC-psbG-ORF157/159 operon of maize plastid
DNA and of the cyanobacterium *Synechocystis* sp. PCC6803.";
Mol. Gen. Genet. 216:60-69(1989).
[2]
SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi I., Matsuno A., Muraki A., Nakazaki N., Nartuo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "sequence analysis of the genome of the unicellular cyanobacterium
RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC
CC -I- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be plastoquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient.
CC -I- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) +
CC plastoquinol.
CC
CC -I- SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.

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CC EMBL; X17439; CAA35486.1; ALT_INIT.
CC EMBL; D90913; BAA18285.1; --
CC PIR; S75826; S75826.
CC InterPro; IPR001268; Complex1_30K.
CC Pfam; PF00329; complex1_30Kd; 1.
CC ProDom; PD001581; Complex1_30K; 1.
CC PROSITE; PS00542; COMPLEX1_30K; 1.
CC Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Complete proteome.
CC SEQUENCE 179 AA; 20593 MW; 3EE18D5E727FBCC CRC64;

Query Match 80.5%; Score 33; DB 1; Length 179;
Best Local Similarity 75.0%; Pred. No. 2.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DY 1 EIRLKVFV 8
DB :|||||:
104 EVRLKVFLL 111

RESULT 12
JUGC ANASP
ID _NUGC ANASP STANDARD; PRT; 175 AA.
DT Q4241; Q5WNN0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase subunit J (EC 1.6.5.-) (NAD(P)H
DE dehydrogenase I, subunit J) (NDH-1, subunit J) (NDH-U).
EN NDHJ OR ALL3840.
ES Anabaena sp. (strain PCC 7120).
XC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
XC NCBI_TaxID=103690;
XN [1]
XN SEQUENCE FROM N.A.
JA Happe T., Schiefer W., Boehme H.;
JA "Isolation and characterisation of the ndhCKJ-cluster of the
JA cyanobacteria *Anabaena* sp. PCC 7120.";
JA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

```

GN NDHJ.
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC9 7937 / ATCC 29413;
RA Happe T., Schiefer W., Boehme H.;
RT "Isolation and characterisation of the ndhCKJ gene-cluster of Anabaena
RL variabilis".
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be plastoquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient (By similarity).
CC CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)H(+) +
CC plastoquinol.
CC CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC DR EMBL; AJ012181; CAB45648.1; -
CC DR InterPro; IPR001268; Complex1_30K.
CC DR Pfam; PF00329; complex1_30K; 1.
CC DR ProDom; PD001591; Complex1_30K; 1.
CC DR PROSITE; PS00542; COMPLEX1_30K; FALSE_NEG.
CC DR Oxidoreductase; NAD; NADP; Quinone; Plastoquinone.
CC KW OXIDOREDUCTASE; NAD; NADP; Quinone; Plastoquinone.
CC SQ SEQUENCE 175 AA; 19949 MW; F902147E12EA1640 CRC64;
Query Match 75.6%; Score 31; DB 1; Length 175;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFV 8
DB 100 EIRKVFV 107
RESULT 14
Y123 THEM
ID Y123 THEM STANDARD; PRT; 267 AA.
AC QWXXY;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Putative periplasmic metal-binding protein TM0123 precursor.
GN TM0123.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGB8 / DSM 3109;
RA MEDLINE=9287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RL genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -1- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM

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CC TM0123/TM0124/TM0125 FOR A METAL. METAL-BINDING COMPONENT.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL SOLUTE-BINDING PROTEIN FAMILY
CC 9.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC EMBL; AB001698; AAD35217.1; -
CC DR PIR; C72415; C72415.
CC DR HSSP; P96116; ITOA.
CC DR TIGR; TM0123; -
CC DR InterPro; IPR006128; Lipoprotein_4.
CC DR InterPro; IPR006127; SBP_bac_9.
CC DR Pfam; PF01297; SBP_bac_9; 1.
CC DR PRINTS; PR00690; ADHESNFAMILY.
CC KW Hypothetical protein; Transport; Periplasmic; Metal-binding; Signal;
CC FT SIGNAL 1 15 POTENTIAL.
CC FT CHAIN 16 267 PUTATIVE PERIPLASMIC METAL-BINDING
CC PROTEIN TM0123.
CC SQ SEQUENCE 267 AA; 30144 MW; 35ADDF6003C22A6 CRC64;
Query Match 75.6%; Score 31; DB 1; Length 267;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIRLKVFV 9
DB 232 EIRKSFV 240
RESULT 15
V07 HPV38
ID V07 HPV38 STANDARD; PRT; 100 AA.
AC Q80308;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human Papillomavirus type 38.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37959;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
CC ACTIVITIES
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC CC EMBL; U31787; AAA79451.1; -
CC DR InterPro; IPR000148; Papvi_E7.
CC DR Pfam; PF00527; E7; 1.
CC KW Early protein; Transcription regulation; Oncogene;
CC DNA-binding; Trans-acting factor.
CC FT SITE 55 58 C-XX-C MOTIF-1.
CC FT SITE 88 91 C-XX-C MOTIF-2.
CC SQ SEQUENCE 100 AA; 11261 MW; C56F5E14A8B978D CRC64;

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Query Match 73.2%; Score 30; DB 1; Length 100;
 Best Local Similarity 62.5%; Pred. No. 6.9;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVYV 8

DB 59 EVRLKLYV 66

Search completed: December 23, 2003, 08:41:54
 Job time : 8.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:58 ; Search time 23.6 Seconds
(without alignments)
98.410 Million cell updates/sec

Title: US-09-989-621-5
Perfect score: 41 EIRLKFVL 9
Sequence: 1 EIRLKFVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacterioph:
17: sp_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	30	12	Q9Q36 hepatitis b
2	41	100.0	30	12	Q9Q33 hepatitis b
3	41	100.0	30	12	Q9Q35 hepatitis b
4	41	100.0	30	12	Q9Q47 hepatitis b
5	41	100.0	30	12	Q9Q40 hepatitis b
6	41	100.0	30	12	Q9Q49 hepatitis b
7	41	100.0	30	12	Q9Q39 hepatitis b
8	41	100.0	30	12	Q9Q50 hepatitis b
9	41	100.0	30	12	Q9Q37 hepatitis b
10	41	100.0	30	12	Q9Q27 hepatitis b
11	41	100.0	30	12	Q9Q30 hepatitis b
12	41	100.0	30	12	Q9Q34 hepatitis b
13	41	100.0	30	12	Q9Q42 hepatitis b
14	41	100.0	31	12	Q67967 hepatitis b
15	41	100.0	31	12	Q8JSB0 hepatitis b
16	41	100.0	31	12	Q8JSB7 hepatitis b

17	41	100.0	31	12	Q67992 hepatitis b
18	41	100.0	31	12	Q68002 hepatitis b
19	41	100.0	31	12	Q68050 hepatitis b
20	41	100.0	31	12	Q68004 hepatitis b
21	41	100.0	31	12	Q68019 hepatitis b
22	41	100.0	31	12	Q68056 hepatitis b
23	41	100.0	31	12	Q68011 hepatitis b
24	41	100.0	31	12	Q8JS66 hepatitis b
25	41	100.0	31	12	Q68071 hepatitis b
26	41	100.0	31	12	Q8JS81 hepatitis b
27	41	100.0	31	12	Q68046 hepatitis b
28	41	100.0	31	12	Q68052 hepatitis b
29	41	100.0	31	12	Q68029 hepatitis b
30	41	100.0	31	12	Q68067 hepatitis b
31	41	100.0	31	12	Q68044 hepatitis b
32	41	100.0	31	12	Q8JSC2 hepatitis b
33	41	100.0	31	12	Q68039 hepatitis b
34	41	100.0	31	12	Q68076 hepatitis b
35	41	100.0	31	12	Q8JSD1 hepatitis b
36	41	100.0	31	12	Q68072 hepatitis b
37	41	100.0	31	12	Q68047 hepatitis b
38	41	100.0	31	12	Q68043 hepatitis b
39	41	100.0	31	12	Q68028 hepatitis b
40	41	100.0	31	12	Q8JSC1 hepatitis b
41	41	100.0	31	12	Q68074 hepatitis b
42	41	100.0	31	12	Q6JSA3 hepatitis b
43	41	100.0	31	12	Q68062 hepatitis b
44	41	100.0	31	12	Q68054 hepatitis b
45	41	100.0	31	12	Q68031 hepatitis b

ALIGNMENTS

RESULT 1

Q9Q36 PRELIMINARY; PRT; 30 AA.
ID Q9Q36
AC Q9Q36;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillion A.P., Norstrom G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106106; AAD46440.1;
DR InterPro; IPR00236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 30
SQ SEQUENCE 30 AA; 3421 MW; 6B4CAB70901228E CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKFVL 9
Db 10 EIRLKFVL 18

RESULT 2

Q9Q53 PRELIMINARY; PRT; 30 AA.
ID Q9Q53
AC Q9Q53;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99169166; PubMed=10068571;
 RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
 RT "Core promoter mutations and genotypes in relation to viral
 RT replication and liver damage in East Asian hepatitis B virus
 RT carriers.";
 RL J. Infect. Dis. 179:775-782(1999).
 DR EMBL; AF106097; AAD46431.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 FT NON TER 30
 FT NON TER 30
 SQ SEQUENCE 30 AA; 3457 MW; 3AA3AB5709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKVFL 9
 DB 10 EIRLKVFL 18

RESULT 3
 Q9QS45 PRELIMINARY; PRT; 30 AA.
 AC Q9QS45
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99169166; PubMed=10068571;
 RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
 RT "Core promoter mutations and genotypes in relation to viral
 RT replication and liver damage in East Asian hepatitis B virus
 RT carriers.";
 RL J. Infect. Dis. 179:775-782(1999).
 DR EMBL; AF106097; AAD46431.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 FT NON TER 30
 FT NON TER 30
 SQ SEQUENCE 30 AA; 3447 MW; 3AA3AB5709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKVFL 9
 DB 10 EIRLKVFL 18

RESULT 4
 Q9QS47 PRELIMINARY; PRT; 30 AA.
 AC Q9QS47
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99169166; PubMed=10068571;
 RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
 RT "Core promoter mutations and genotypes in relation to viral
 RT replication and liver damage in East Asian hepatitis B virus
 RT carriers.";
 RL J. Infect. Dis. 179:775-782(1999).
 DR EMBL; AF106097; AAD46429.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 FT NON TER 30
 FT NON TER 30
 SQ SEQUENCE 30 AA; 3447 MW; 3AA3AB5709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKVFL 9
 DB 10 EIRLKVFL 18

RESULT 5
 Q9QS40 PRELIMINARY; PRT; 30 AA.
 AC Q9QS40
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99169166; PubMed=10068571;
 RA Lindh M., Hannoun C., Dhillion A.P., Norrkans G., Horal P.;
 RT "Core promoter mutations and genotypes in relation to viral
 RT replication and liver damage in East Asian hepatitis B virus
 RT carriers.";
 RL J. Infect. Dis. 179:775-782(1999).
 DR EMBL; AF106102; AAD46436.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON TER 1
 FT NON TER 30
 FT NON TER 30
 SQ SEQUENCE 30 AA; 3447 MW; 3AA3AB5709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKVFL 9
 DB 10 EIRLKVFL 18

RESULT 6
 Q9QS19 PRELIMINARY; PRT; 30 AA.
 AC Q9QS19
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.

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OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106123; AAD46457.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
FT NON_TER 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18

RESULT 7
Q9QS29
ID Q9QS29 PRELIMINARY; PRT; 30 AA.
AC Q9QS29;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106113; AAD46447.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
FT NON_TER 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18

RESULT 8
Q9QS50
ID Q9QS50 PRELIMINARY; PRT; 30 AA.
AC Q9QS50;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106092; AAD46426.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
FT NON_TER 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18

RESULT 9
Q9QS37
ID Q9QS37 PRELIMINARY; PRT; 30 AA.
AC Q9QS37;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers.";
RL J. Infect. Dis. 179:775-782(1999).
DR EMBL; AF106105; AAD46439.1; -
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1
FT NON_TER 30
FT NON_TER 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 10 EIRLKVFL 18

RESULT 10
Q9QS27
ID Q9QS27 PRELIMINARY; PRT; 30 AA.
AC Q9QS27;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral

```

RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).
DR ENBL, AF106115, AAD46449.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
| | | | |
Db 10 EIRLKVFL 18

RESULT 11

Q9QS30 PRELIMINARY; PRT; 30 AA.
AC Q9QS30;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).
DR ENBL; AF106112; AAD46446.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3460 MW; 3AA3ACB607E1CD98 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
| | | | |
Db 10 EIRLKVFL 18

RESULT 12

Q9QS44 PRELIMINARY; PRT; 30 AA.
AC Q9QS44;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).

DR ENBL; AF106098; AAD46432.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
| | | | |
Db 10 EIRLKVFL 18

RESULT 13

Q9QS42 PRELIMINARY; PRT; 30 AA.
AC Q9QS42;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169166; PubMed=10068571;
RA Lindh M., Hannoun C., Dhillon A.P., Norrkans G., Horal P.;
RT "Core promoter mutations and genotypes in relation to viral
RT replication and liver damage in East Asian hepatitis B virus
RT carriers."
RL J. Infect. Dis. 179:775-782(1999).
DR ENBL; AF106100; AAD46434.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3447 MW; 3AA3ACB709012298 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
| | | | |
Db 10 EIRLKVFL 18

RESULT 14

Q67967 PRELIMINARY; PRT; 31 AA.
AC Q67967;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE X, PreC and C genes (Pintus) (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retrovirdae; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the ENBL/GenBank/DBJ databases.
DR ENBL; X85287; CAA59548.1; -.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 1 1
FT NON_TER 31 AA; 3364 MW; A776AB25508DEA72 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred.No. 0.062; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
 | | | | |
 Db 3 EIRLKVFL 11

RESULT 15

28JSB0 PRELIMINARY; PRT; 31 AA.
 ID Q8JSB0
 AC Q8JSB0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE X protein (Fragment).
 OS Hepatitis B virus.
 NC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
 CX NCBI_TaxID=10407;
 XN [1]
 XP SEQUENCE FROM N.A.
 RC STRAIN=23;
 XX PubMed=12185284;
 YA Hou J., Lin Y., Waters J., Wang Z., Min J., Liao H., Jiang J.,
 XT "Detection and significance of a G1862T variant of hepatitis B virus
 XT in Chinese patients with fulminant hepatitis.";
 RL J. Gen. Virol. 83:2291-2298(2002).
 DR EMBL; AF495684; ANM34071.1; -.
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 PT NON TER 1
 IQ SEQUENCE 31 AA; 3380 MW; A776BDF508DEA72 CRC64;

Query Match 100.0%; Score 41; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred.No. 0.062; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 EIRLKVFL 9
 | | | | |
 Db 3 EIRLKVFL 11

earch completed: December 23, 2003, 08:46:13
 ob time : 25.6 secs


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; Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVL 9
   |||||
Db 1 EIRLKFVL 9

RESULT 2
US-09-051-006-5
; Sequence 5, Application US/09051006
; Patent No. 6380359
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Young
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; FILE REFERENCE: 0136/08154
; CURRENT APPLICATION NUMBER: US/09/051,006
; CURRENT FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-051-006-5

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVL 9
   |||||
Db 1 EIRLKFVL 9

RESULT 3
5204446-1
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:1
; LENGTH: 24
5204446-1

Query Match 100.0%; Score 41; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVL 9
   |||||
Db 13 EIRLKFVL 21

RESULT 4
5204446-3
; Patent No. 5204446
; APPLICANT: KUMAZAWA, TOSHIKI;OSANAI, MASATOSHI
; TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
; WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
; NUMBER OF SEQUENCES: 4
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/503,239
; FILING DATE: 02-APR-1990
; SEQ ID NO:3
; LENGTH: 24
5204446-3

Query Match 100.0%; Score 41; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVL 9
   |||||
Db 13 EIRLKFVL 21

RESULT 5
US-08-319-376-5
; Sequence 5, Application US/08319376
; Patent No. 5872286
; GENERAL INFORMATION:
; APPLICANT: Liang, Tsanyang J
; APPLICANT: Huang, Jiakang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INTERFERING
; WITH HEPATITIS B VIRUS INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,376
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: MGH-126XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-319-376-5

Query Match 100.0%; Score 41; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.046; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 EIRLKFVL 9
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Db 16 EIRLKFVL 24

RESULT 6
5196194-20
; Patent No. 5196194
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APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,621
FILING DATE: 7-DEC-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 513,055
FILING DATE: 12-JUL-1983
APPLICATION NUMBER: 107,267
FILING DATE: 21-DEC-1979
APPLICATION NUMBER: 41,909
FILING DATE: 24-MAY-1979
SEQ ID NO:20:
LENGTH: 153
5196194-20

Query Match 100.0%; Score 41; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134

RESULT 7
5204446-4
Patent No. 5204446
APPLICANT: KIMAZAWA, TOSHIKI; OSANAI, MASATOSHI
TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/503,239
FILING DATE: 02-APR-1990
SEQ ID NO:4:
LENGTH: 153
5204446-4

Query Match 100.0%; Score 41; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 125 EIRLKVFL 133

RESULT 8
5183734-1
Patent No. 5183734
APPLICANT: MORIARTY, ANN M.
TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS
FOR ASSAYING SV40 HBXAG
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,982
FILING DATE: 17-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 54,424
FILING DATE: 26-MAY-1987
APPLICATION NUMBER: 648,142
FILING DATE: 07-SEP-1984
APPLICATION NUMBER: 587,570
FILING DATE: 08-MAR-1984
SEQ ID NO:1:
LENGTH: 154
5183734-1

Query Match 100.0%; Score 41; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134

RESULT 9
US-09-719-528A-5
Sequence 5, Application US/09719528A
Patent No. 6558675
GENERAL INFORMATION:
APPLICANT: Oon, Chong Jin
Lim, Gek Keow
Zhao, Yi
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-APR-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-719-528A-5

Query Match 90.2%; Score 37; DB 4; Length 154;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 126 EIRLKVFL 134

RESULT 10
5204446-2
Patent No. 5204446
APPLICANT: KIMAZAWA, TOSHIKI; OSANAI, MASATOSHI
TITLE OF INVENTION: POLYPEPTIDE HAVING IMMUNOREACTIVITY
WITH ANTIBODY SPECIFIC TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/503,239
FILING DATE: 02-APR-1990
SEQ ID NO:2:
LENGTH: 24

5204446-2

Query Match 82.9%; Score 34; DB 6; Length 24;
 Best Local Similarity 77.8%; Pred. No. 0.91;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLKVFVL 9
 |||||:||||
 Db 13 EIRLMIFVL 21

RESULT 11

US-08-818-112-65
 ; Sequence 65, Application US/08818112
 ; Patent No. 6290969
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Houghton, Raymond
 ; APPLICANT: Twardzik, Daniel R.
 ; APPLICANT: Twardzik, Daniel R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 13-MAR-1997
 ; APPLICATION NUMBER: US/08/818,112
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.41106
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

US-08-818-112-65
 Query Match 75.6%; Score 31; DB 3; Length 230;
 Best Local Similarity 44.4%; Pred. No. 37;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKVFVL 9
 |||||:||||
 Db 66 DVRKIFVL 74

RESULT 12

US-08-818-111-66
 ; Sequence 66, Application US/08818111
 ; Patent No. 6338852
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Twardzik, Daniel R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 TUBERCULOSIS
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 13-MAR-1997
 ; APPLICATION NUMBER: US/08/818,111
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.417C6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 66:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

US-08-818-111-66
 Query Match 75.6%; Score 31; DB 4; Length 230;
 Best Local Similarity 44.4%; Pred. No. 37;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKVFVL 9
 |||||:||||
 Db 66 DVRKIFVL 74

RESULT 13

US-09-056-556-65
 ; Sequence 65, Application US/09056556
 ; Patent No. 6350456
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
 TREAT
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/056,556
 ; FILING DATE: 07-APR-1998
 ; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-65

Query Match 75.6%; Score 31; DB 4; Length 230;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
DB 66 DVRKIFML 74

RESULT 14
US-09-072-596-65
Sequence 66, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-65

Query Match 75.6%; Score 31; DB 4; Length 230;
Best Local Similarity 44.4%; Pred. No. 37;

Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKVFL 9
DB 66 DVRKIFML 74
RESULT 15
US-09-107-532A-5314
Sequence 5314, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5314:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...540
SEQUENCE DESCRIPTION: SEQ ID NO: 5314;
US-09-107-532A-5314

Query Match 73.2%; Score 30; DB 4; Length 540;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 7
DB 440 EIRLKVFL 446

Search completed: December 23, 2003, 08:53:52
Job time : 11.6 secs

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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 6.4 Seconds
(without alignments)

66.131 Million cell updates/sec

Title: US-09-989-621-1

Perfect score: 45

Sequence: 1 HLSIRGLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	154	1 X HPEV4	P12836 hepatitis b
2	37	82.2	1436	1 WC11_BOVIN	P30205 bos taurus
3	35	77.8	154	1 X HPEV2	P30166 hepatitis b
4	35	77.8	154	1 X HPEV9	P17102 hepatitis b
5	35	77.8	154	1 X HPEV4	P24026 hepatitis b
6	35	77.8	154	1 X HPEV1	P20976 hepatitis b
7	35	77.8	154	1 X HPEVJ	P20976 hepatitis b
8	35	77.8	154	1 X HPEVJ	P12912 hepatitis b
9	35	77.8	154	1 X HPEVO	P20977 hepatitis b
10	35	77.8	154	1 X HPEVJ	P03165 hepatitis b
11	35	77.8	154	1 X HPEVJ	P23161 clostridium
12	34	75.6	178	1 P20K_CLOPA	P29585 methanobact
13	34	75.6	361	1 P20K_METTF	P30048 homo sapien
14	33	73.3	256	1 PDX3_HUMAN	P35705 bos taurus
15	33	73.3	257	1 PDX3_BOVIN	P56900 rhizobium m
16	33	73.3	695	1 TKT2_RHIME	Q9rx14 deinococcus
17	32	71.1	369	1 PYRD_DEIRA	P12704 escherichia
18	32	71.1	430	1 YJCF_ECOLI	Q960a0 caenorhabdi
19	32	71.1	628	1 YS9A_CASEL	P31423 sheep pulmo
20	32	71.1	870	1 POL_TSRV	Q8k320 mus musculu
21	32	71.1	1020	1 CARE_MOUSE	Q14690 homo sapien
22	32	71.1	1884	1 RRP5_HUMAN	P04114 homo sapien
23	32	71.1	4563	1 APB_HUMAN	Q8t564 echinococcu
24	31	68.9	193	1 TDX_ECHGR	Q04120 saccharomyc
25	31	68.9	195	1 TSA2_YEAST	Q56624 synechocyst
26	31	68.9	200	1 V755_SINY3	Q95468 hordeum vul
27	31	68.9	210	1 BAS1_HORVJ	P80602 triticum ae
28	31	68.9	210	1 BAS1_WHEAT	P20108 mus musculu
29	31	68.9	257	1 PDX3_MOUSE	Q24364 spinacia ol
30	31	68.9	265	1 BAS1_SPIOL	Q96291 arabidopsis
31	31	68.9	266	1 BAS1_ARATH	Q57891 methanococc
32	31	68.9	361	1 Y439_METJA	P29584 methanobact
33	31	68.9	361	1 YPVB_METTF	

RESULT 1

X HPEV4
ID X HPEV4 STANDARD; PRT; 154 AA.
AC P12935; 1992 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DR 01-OCT-1989 (Rel. 12, Last sequence update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyanchara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
CC - FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
CC
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CC
CC EMBL; X01587; CAA25744.1; -
CC InterPro; IPR000236; TransactX.
CC Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16622 MW; 594A1D0718928804 CRC64;

Query Match 100.0%; Score 45; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLSIRGLFV 9

DB 52 HLSIRGLFV 60

RESULT 2

WC11_BOVIN
ID WC11_BOVIN STANDARD; PRT; 1436 AA.
AC P30205;
DT 01-APR-1993 (Rel. 25, Created)
DR 01-APR-1993 (Rel. 25, Last sequence update)
DE Trans-activating protein X.
GN X.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
 [1] X_HPBV2 STANDARD; PRT; 154 AA.
 AC P03166; P12935;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DB Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw2), and
 OS Hepatitis B virus (subtype adw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OC NCBI_TaxID=10408, 106821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW2;
 RA Valenzuela P., Quiroga M., Zaidivar J., Gray P., Rutter W.J.;
 RA (in) Field B.N., Jaenisch R., Fox C.P. (eds.);
 RA Animal virus genetics, pp.57-70, Academic Press, New York (1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW;
 RX MEDLINE=89045656; PubMed=6300776;
 RA Ono Y., Onda H., Sasaki R., Igarashi K., Sugino Y., Nishioka K.;
 RA "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA; subtype adr and adw";
 RT Nucleic Acids Res. 11:1747-1757(1983).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC -----
 CC EMBL; X02763; CA226540.1; -;
 CC EMBL; Z35717; CA84789.1; -;
 CC EMBL; M23692; AA56820.1; -;
 CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
 CC PIR; A31283; QQVLAW.
 CC PIR; S47408; S47408.
 CC InterPro; IPR000236; TransactX.
 CC Pfam; PF00739; X; 1; 80 E -> A (IN REF. 3).
 CC CONFLICT 80 80
 CC CONFLICT 115 115 C -> S (IN REF. 2).
 CC CONFLICT 130 131 KV -> MI (IN REF. 3).
 CC SEQUENCE 154 AA; 16993 MW; 7F2AE32A4F025670 CRC64;
 Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSLRGL 7
 DB 52 HSLRGL 58
 RESULT 4
 X_HPBV9 STANDARD; PRT; 154 AA.
 AC P17102;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.

NCBI_TaxID=9913;
 [1] X_HPBV2 STANDARD; PRT; 154 AA.
 AC P03166; P12935;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DB Trans-activating protein X.
 GN X.
 OS Hepatitis B virus (subtype adw2), and
 OS Hepatitis B virus (subtype adw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OC NCBI_TaxID=10408, 106821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW2;
 RA Valenzuela P., Quiroga M., Zaidivar J., Gray P., Rutter W.J.;
 RA (in) Field B.N., Jaenisch R., Fox C.P. (eds.);
 RA Animal virus genetics, pp.57-70, Academic Press, New York (1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADW;
 RX MEDLINE=89045656; PubMed=6300776;
 RA Ono Y., Onda H., Sasaki R., Igarashi K., Sugino Y., Nishioka K.;
 RA "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA; subtype adr and adw";
 RT Nucleic Acids Res. 11:1747-1757(1983).
 CC -1- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
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 CC -----
 CC EMBL; X02763; CA226540.1; -;
 CC EMBL; Z35717; CA84789.1; -;
 CC EMBL; M23692; AA56820.1; -;
 CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
 CC PIR; A31283; QQVLAW.
 CC PIR; S47408; S47408.
 CC InterPro; IPR000236; TransactX.
 CC Pfam; PF00739; X; 1; 80 E -> A (IN REF. 3).
 CC CONFLICT 80 80
 CC CONFLICT 115 115 C -> S (IN REF. 2).
 CC CONFLICT 130 131 KV -> MI (IN REF. 3).
 CC SEQUENCE 154 AA; 16993 MW; 7F2AE32A4F025670 CRC64;
 Query Match 77.8%; Score 35; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSLRGL 7
 DB 52 HSLRGL 58
 RESULT 4
 X_HPBV9 STANDARD; PRT; 154 AA.
 AC P17102;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Trans-activating protein X.

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CC -----
DR EMBL; D00329; -; NOT_ANNOTATED_CDS.
DR PIR; J50256; JS0256;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16585 MW; 512A5A077169D5CA CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
Db 52 HLSRGL 58

RESULT 8
X_HPBVL STANDARD; PRT; 154 AA.
AC P12912;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.

OS Hepatitis B virus (strain Ish / chimpanzee isolate).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaadin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee."
RL J. Gen. Virol. 69:1383-1389(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----
DR EMBL; D00220; BAA00160.1; -;
DR PIR; D28885; QQVLCF.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16759 MW; F6C9D7D30C16D743 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
Db 52 HLSRGL 58

RESULT 9
X_HPBVO STANDARD; PRT; 154 AA.
AC P20977;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype adw / strain Okinawa/PODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastroewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes."
RL J. Gen. Virol. 69:2575-2583(1988).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----
DR EMBL; D00330; -; NOT_ANNOTATED_CDS.
DR PIR; J50603; JS0603.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16558 MW; E2646C059A30125F CRC64;

Query Match 77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
Db 52 HLSRGL 58

RESULT 10
X_HPBVT STANDARD; PRT; 154 AA.
AC Q05499;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Trans-activating protein X.
GN X.

OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4."
RL J. Gen. Virol. 74:1627-1632(1993).
CC -!- FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.

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CC -----
DR EMBL; X69798; CAA49453.1; -;
DR PIR; J02228; J02228.
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
SQ SEQUENCE 154 AA; 16715 MW; B523C051B9B0B737 CRC64;

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Query Match      77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLSRGL 7
DB 52 HLSRGL 58

RESULT 11
X_HPBVV STANDARD; PRT; 154 AA.
AC P03165;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-activating protein X.
GN X.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Piteussel F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
RT cloned in E. coli.";
RL Nature 281:646-650(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Latvia;
RX MEDLINE=85204397; PubMed=3996597;
RA Bicko V., Dreilina D., Pushko P.M., Pumpen P.P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
RT analysis.";
RL FEBS Lett. 185:208-212(1985).
XC - FUNCTION: INDISPENSABLE FOR HBV REPLICATION IN VIVO.
XC
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XC or send an email to license@isb-sib.ch).
XC
XC EMBL; V01460; -; NOT ANNOTATED_CDS.
XR EMBL; X02496; CAB41637.1; -;
RR PIR; A03719; QOVLDI.
RR PIR; A05237; QOVLBI.
RR InterPro; IPR00236; TransactX.
RR Pfam; PF00733; X; 1.
R T VARIANT 46 46 P -> S (IN STRAIN LATVIA).
R T VARIANT 84 88 NAHQI -> KAQPF (IN STRAIN LATVIA).
R T VARIANT 102 102 A -> V (IN STRAIN LATVIA).
R T CONFLICT 26 26 R -> C (IN REF. 1).
Q SEQUENCE 154 AA; 16618 MW; 29FDICCE09A34B5 CRC64;

Query Match      77.8%; Score 35; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 HLSRGL 7
b 52 HLSRGL 58

RESULT 12
20K_CLOPA STANDARD; PRT; 178 AA.
D R20K_CLOPA
C P23161;
T 01-NOV-1991 (Rel. 20, Created)

```

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DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 20 kDa protein in rubredoxin operon (ORF C).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92344580; PubMed=1637309;
RA Mathieu I., Meyer J., Moulis J.M.;
RT "Cloning, sequencing and expression in Escherichia coli of the
RT rubredoxin gene from Clostridium pasteurianum.";
RL Biochem. J. 285:255-262(1992).
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M60116; AAA23278.1; -;
DR PIR; S29119; S29119.
DR HSSP; P30041; IPRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
KW Oxidoreductase.
FT ACT SITE 50 50 BY SIMILARITY.
FT ACT_SITE 167 167 BY SIMILARITY.
SQ SEQUENCE 178 AA; 20036 MW; DP9AD3D8F1B93A64 CRC64;

Query Match      75.8%; Score 34; DB 1; Length 178;
Best Local Similarity 75.0%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSLRGLFV 9
DB 123 ISLGRUFI 130

RESULT 13
YPZ8 METTF STANDARD; PRT; 361 AA.
AC P29585;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Hypothetical 40.6 kDa protein (ORF8').
OS Methanobacterium thermoformicicum.
OG Plasmid pFZ1.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3720 / 2-245;
RX MEDLINE=93126090; PubMed=1336177;
RA Noelling J., van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;
RT "Modular organization of related Archaeal plasmids encoding different
RT restriction-modification systems in Methanobacterium
RT thermoformicicum.";
RL Nucleic Acids Res. 20:6501-6507(1992).
CC -1- SIMILARITY: TO THE CORRESPONDING ORF IN PFV1.
CC
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CC  -----
CC  EMBL; X68367; CAA48439.1; -.
CC  PIR; S30325; S30325.
CC  KW  Hypothetical protein; Plasmid.
CC  SQ  SEQUENCE 361 AA; 40565 MW; 5787C9D090AG384F CRC64;
CC
CC  Query Match 75.6%; Score 34; DB 1; Length 361;
CC  Best Local Similarity 87.5%; Pred. No. 8.7;
CC  Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC  Qy 1 HSLRGLFV 8
CC  |||||
CC  223 HSLRGLFV 230
CC
CC  Db
CC
CC  RESULT 14
CC  ID PDX3_HUMAN
CC  AC P30048; P35690; Q13776; Q96HK4; PRT; 256 AA.
CC  DT 01-APR-1993 (Rel. 25, Created)
CC  DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC  DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC  DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor
CC  DE (EC 1.1.1.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MERS
CC  DE protein homolog) (HBC189) (PRX III).
CC  GN PRDX3 OR AOP1
CC  OS Homo sapiens (Human).
CC  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC  OX NCBI_TaxID=9606;
CC  RN [1]
CC  RP SEQUENCE FROM N.A.
CC  RC TISSUE=Blood;
CC  RX MEDLINE=95251598; PubMed=7733872;
CC  RA Tsuji K., Copeland N.G., Jenkins N.A., Obinata M.;
CC  RT "Mammalian antioxidant protein complements alkylhydroperoxide
CC  RT reductase (ahpC) mutation in Escherichia coli.";
CC  RL Biochem. J. 307:377-381(1995).
CC  RN [2]
CC  RP SEQUENCE FROM N.A.
CC  RC TISSUE=Skin, Testis, Urinary bladder, and Uterus;
CC  RX MEDLINE=22388257; PubMed=12477932;
CC  RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC  RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC  RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC  RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC  RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC  RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC  RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
CC  RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
CC  RA Bosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,
CC  RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
CC  RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC  RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
CC  RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
CC  RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC  RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC  RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,
CC  RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
CC  RT "Generation and initial analysis of more than 15,000 full-length
CC  RT human and mouse cDNA sequences.";
CC  RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  RN [3]
CC  RP SEQUENCE OF 148-240 FROM N.A.
CC  RX MEDLINE=94108427; PubMed=7506601;
CC  RA Takeda J., Yano H., Eng S., Zeng Y., Bell G.I.;
CC  RT "A molecular inventory of human pancreatic islets: sequence analysis
CC  RT of 1000 cDNA clones.";
CC  RN Hum. Mol. Genet. 2:1793-1798(1993).
CC  RN [4]
CC  RP SEQUENCE OF 63-72.
CC  RT TISSUE=Liver;

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RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tisot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [5]
RP OVEROXIDATION OF CYS-108.
RX MEDLINE=22201787; PubMed=12059788;
RA Wagner E., Lucie S., Penna L., Chevallet M., van Dorsselaer A.,
RA Leize-Wagner E., Rabilloud T.;
RT "A method for detection of overoxidation of cysteines: peroxiredoxins
RT are oxidized in vivo at the active-site cysteine during oxidative
RT stress.";
RL Biochem. J. 366:777-785(2002).
CC -!- FUNCTION: Involved in redox regulation of the cell. Protects
CC radical-sensitive enzymes from oxidative damage by a radical-
CC generating system.
CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: The active site is the redox-active Cys-108
CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-229-SH of the
CC other subunit to form an intermolecular disulfide with a
CC concomitant homodimer formation. The enzyme may be subsequently
CC regenerated by reduction of the disulfide by thioredoxin.
CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-108
CC (to Cys-SO3H) upon oxidative stress.
CC -!- SIMILARITY: BELONGS TO THE AHP/TSA FAMILY.
CC -----
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CC -----
CC EMBL; D49396; BAA08389.1; -.
CC EMBL; BC002685; AAH02685.1; -.
CC EMBL; BC008038; AAH08038.1; -.
CC EMBL; BC008435; AAH08435.1; -.
CC EMBL; BC021691; AAH21691.1; -.
CC EMBL; BC022373; AAH22373.1; -.
CC EMBL; T10952; -. NOT ANNOTATED_CDS.
CC SWISS-2DPAGE; P30048; HUMAN.
CC Sigena-2DPAGE; P30048; -.
CC Genew; HGNC:9354; PRDX3.
CC MIN; 604769; -.
CC GO; GO:0008785; F:alkyl hydroperoxide reductase activity; TAS.
CC InterPro; IPR000866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
CC Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
CC Mitochondrion; Transit peptide.
CC TRANSIT 1 62 MITOCHONDRION.
CC CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
CC ACT_SITE 108 108 CYSTEINE SULFENIC ACID INTERMEDIATE
CC (BY SIMILARITY)
CC DISULFID 108 108 INTERCHAIN (WITH C-229) (IN
CC LINKED FORM) (BY SIMILARITY).
CC DISULFID 229 229 INTERCHAIN (WITH C-108) (IN
CC LINKED FORM) (BY SIMILARITY).
CC CONFLICT 31 31 R -> W (IN REF. 2; AAH08435).
CC SEQUENCE 256 AA; 27692 MW; 8BB7F5E55BFE9BE CRC64;
CC
CC Query Match 73.3%; Score 33; DB 1; Length 256;
CC Best Local Similarity 75.0%; Pred. No. 10;
CC Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 2 LSLRGLFV 9
CC |||||
CC 181 LALRGLFI 188
CC
CC Db

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RESULT 15
 D PDX3_BOVIN STANDARD; PRT; 257 AA.
 C P35705;
 T 01-JUN-1994 (Rel. 29, Created)
 T 01-NOV-1997 (Rel. 35, Last sequence update)
 T 15-SEP-2003 (Rel. 42, Last annotation update)
 E Thioresoxin-dependent peroxide reductase, mitochondrial precursor
 E (EC 1.1.1.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (SP-22
 E protein).
 S Bos taurus (Bovine).
 S Bos taurus (Bovine).
 S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 S Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 S Bovidae; Bovinae; Bos.
 C NCBI_TaxID=9913;
 C [1]
 N SEQUENCE FROM N.A.
 N TISSUE=Adrenal medulla;
 P MEDLINE=97069947; PubMed=8912927;
 C Hiroi T., Watabe S., Takimoto K., Yago N., Ymanoto Y., Takahashi S.Y.;
 X "The cDNA sequence encoding bovine SP-22, a new defence system
 T against reactive oxygen species in mitochondria.";
 T DNA Seq. 6:239-242(1996).
 L [2]
 P SEQUENCE OF 2-257 FROM N.A.
 P TISSUE=Adrenal medulla;
 C MEDLINE=94375407; PubMed=8089078;
 X Watabe S., Kono H., Kouyama H., Hiroi T., Yago N., Nakazawa T.;
 A "Purification and characterization of a substrate protein for
 T mitochondrial ATP-dependent protease in bovine adrenal cortex.";
 T J. Biochem. 115:648-654(1994).
 L -!- FUNCTION: Involved in redox regulation of the cell. Protects
 C radical-sensitive enzymes from oxidative damage by a radical-
 C generating system.
 C -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
 C similarity).
 C -!- SUBCELLULAR LOCATION: Mitochondrial.
 C -!- MISCELLANEOUS: The active site is the redox-active Cys-109
 C oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the
 C other subunit to form an intermolecular disulfide with a
 C concomitant homodimer formation. The enzyme may be subsequently
 C regenerated by reduction of the disulfide by thioredoxin (By
 C similarity).
 C -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-109
 C (to Cys-SO3H) upon oxidative stress (By similarity).
 C -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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EMBL; D82025; BAA11511.1; -
 HSSP; P30041; 1PRX.
 InterPro; IPR000866; Ahpc-TSA.
 Pfam; PF00578; Ahpc-TSA; 1.
 Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
 Mitochondrion; Transmembrane protein.
 TRANSIT 1 63
 CHAIN 64 257
 ACT_SITE 109 109
 DISULFID 109 109
 DISULFID 230 230
 SEQUENCE 257 AA; 28195 MW; F2E89EE2F172A42D CRC64;
 MITOCHONDRION (BY SIMILARITY).
 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
 CYSTEINE SULFENIC ACID INTERMEDIATE
 (BY SIMILARITY).
 INTERCHAIN (WITH C-230) (IN
 LINKED FORM) (BY SIMILARITY).
 INTERCHAIN (WITH C-109) (IN
 LINKED FORM) (BY SIMILARITY).
 SEQUENCE 257 AA; 28195 MW; F2E89EE2F172A42D CRC64;

Query Match 73.3%; Score 33; DB 1; Length 257;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LSURGLFV 9
 Db 182 LALRGLFI 189
 Search completed: December 23, 2003, 08:41:44
 Job time : 9.4 secs

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M protein - protein search, using sw model

run on: December 23, 2003, 08:39:57, Search time 25.8 Seconds
(without alignments)
55,370 Million cell updates/sec

title: US-09-989-621-3

effect score: 42

sequence: 1 AMSTTDLEA 9

coring table: BLOSUM62
Gapop 10.0, Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database: A_Geneseq_19Jun03.*

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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	42	100.0	9	20	AAV24461
2	42	100.0	9	23	ABJ05975
3	42	100.0	9	23	ABJ07513
4	42	100.0	15	6	AAV20458
5	42	100.0	15	23	ABJ08978
6	42	100.0	15	23	ABJ09270
7	42	100.0	16	9	AAV202170
8	42	100.0	134	16	AAV71563
9	42	100.0	154	6	AAV50461

10	42	100.0	154	9	AAV24461	Peptide encoded by
11	42	100.0	154	21	AAV58473	Hepatitis B virus
12	42	100.0	154	21	AAV54047	Amino acid sequence
13	42	100.0	154	21	AAV44351	Human hepatitis B
14	38	90.5	8	23	ABJ07178	Hepatitis B virus
15	38	90.5	8	23	ABJ08117	Hepatitis B virus
16	38	90.5	9	15	AAV38029	Hepatitis B virus
17	38	90.5	9	20	AAV45599	Immunogenic peptide
18	38	90.5	9	21	AAV73060	Immunogenic peptide
19	38	90.5	9	22	AAV20241	Hepatitis C virus
20	38	90.5	9	23	ABJ05903	Hepatitis B virus
21	38	90.5	9	23	ABJ07244	Hepatitis B virus
22	38	90.5	9	23	ABJ07856	Hepatitis B virus
23	38	90.5	9	23	ABJ08118	Hepatitis B virus
24	38	90.5	9	23	ABJ08480	Hepatitis B virus
25	38	90.5	9	23	ABJ08831	Hepatitis B virus
26	38	90.5	9	23	ABJ09123	Hepatitis B virus
27	38	90.5	9	23	ABJ09849	Hepatitis B virus
28	38	90.5	10	23	ABJ07301	Hepatitis B virus
29	38	90.5	10	23	ABJ08119	Hepatitis B virus
30	38	90.5	11	23	ABJ06438	Hepatitis B virus
31	38	90.5	11	23	ABJ08120	Hepatitis B virus
32	38	90.5	11	23	ABJ08481	Hepatitis B virus
33	36	85.7	9	23	ABJ07896	Hepatitis B virus
34	34	81.0	7	23	ABJ05904	Hepatitis B virus
35	33	78.6	8	22	AAV20248	Hepatitis B virus
36	33	78.6	8	23	ABJ05935	Hepatitis B virus
37	33	78.6	8	23	ABJ06836	Hepatitis B virus
38	33	78.6	8	23	ABJ07197	Hepatitis B virus
39	33	78.6	8	23	ABJ07863	Hepatitis B virus
40	33	78.6	8	23	ABJ08243	Hepatitis B virus
41	33	78.6	8	23	ABJ08547	Hepatitis B virus
42	33	78.6	9	23	ABJ05936	Hepatitis B virus
43	33	78.6	9	23	ABJ06837	Hepatitis B virus
44	33	78.6	9	23	ABJ07260	Hepatitis B virus
45	33	78.6	9	23	ABJ08244	Hepatitis B virus

ALIGNMENTS

RESULT 1

AAV24461
ID AAV24461 standard; peptide; 9 A.

XX
AC AAV24461;

XX
DT 23-SEP-1999 (first entry)

XX
DE Hepatitis B virus X protein peptide #3.

XX
KW Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;
CTL; antigen; immunity; liver cancer.

XX
OS Hepatitis B virus.

XX
OS Synthetic.

XX
PN WO9396434-A1.

XX
PD 22-JUL-1999.

XX
PF 19-JAN-1998; 98WO-KR00010.

XX
PR 19-JAN-1998; 98WO-KR00010.

XX
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

XX
PI Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;

XX
PI Lee K;

XX
DR WPI; 1999-444387/37.

XX
PI Hepatitis B virus protein X-derived peptide antigens used to

PT stimulate cytotoxic T lymphocytes, useful for treatment of
 XX HBV-associated diseases, especially liver cancer
 PS Claim 3; Page 24; 33pp; English.

CC The present invention describes peptide antigens AAY24459 to AAY24463
 CC derived from the X protein of hepatitis B virus (HBV) which are
 CC recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CC derived from HBV X protein are useful for inducing CTLs against the
 CC virus or inducing immunological tolerance to the virus. pH-sensitive
 CC liposomes containing the peptide antigens are used to induce cellular
 CC immunity so that CTLs specific to the virus can be produced. This is
 CC useful for prevention and treatment of HBV-associated diseases,
 CC especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CC the selective transportation of anti-cancer drugs.

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 1 AMSTTDLEA 9
 DB 1 AMSTTDLEA 9

RESULT 2
 ABJ05975
 ID ABJ05975 standard; Peptide; 9 AA.

AC ABJ05975;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #193.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 Celis E, Kubo RT, Grey HM, Chesnut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -

Disclosure; Page 113; 228pp; English.

The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;

Query Match 100.0%; Score 42; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 DB 1 AMSTTDLEA 9

RESULT 3

ID ABJ07513 standard; Peptide; 9 AA.

AC ABJ07513;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #1731.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 Celis E, Kubo RT, Grey HM, Chesnut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -

Disclosure; Page 145; 228pp; English.

The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;

Query Match 100.0%; Score 42; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 DB 1 AMSTTDLEA 9

RESULT 4

AAP50458

ID AAP50458 standard; Protein; 15 AA.

AC AAP50458;

25-MAR-2003 (updated)

27-SEP-1991 (first entry)

Sequence of an antigenic determinant of HBxAg, the antigen
 encoded by the X region of the hepatitis B virus genome.

PI Celis E, Kubo RT, Grey HM, Chesnut RW;
XX WPI; 2002-643192/69.
XX
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -
XX
XX Disclosure; Page 179; 228pp; English.
PS
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 42; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 AMSTTDLEA 9
 |||||||
Db 3 AMSTTDLEA 11

RESULT 6
ABJ09270
ID ASJ09270 standard; Peptide; 15 AA.
XX
XX AC ABJ09270;
XX
DT 14-NOV-2002 (first entry)
XX
DE Hepatitis B virus epitope #3498.
XX
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KW virucide; hepatotropic; antiinflammatory.
XX
OS Hepatitis B virus.
XX
PN WO200219986-A1.
XX
PD 14-MAR-2002.
XX
PF 08-SEP-2000; 2000WO-US24802.
XX
XX 08-SEP-2000; 2000WO-US24802.
PR
PA (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
PI Sette A, Sidnev J, Southwood S, Vitiello MA, Livingstone BD;
PI Celis E, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/69.
XX
PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -
XX
XX Disclosure; Page 182; 228pp; English.
PS
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 42; DB 23; Length 15;

R 08-MAR-1984; 84US-0587570.
 R 26-MAY-1987; 87US-0054424.
 X A (SCRI) SCRIPPS CLINIC & RES FOUND.
 X Moriarty AM, Alexander H, Lerner RA;
 R WPI; 1985-236420/38.
 R Expression vector contg. gene coding for hepatitis B HBxAg -
 T useful in diagnostic systems for detection of HBxAg and its
 T antibody in body samples
 S Disclosure; Fig 6; 86pp; English.
 X The inventors claim an antigenic synthetic polypeptide containing
 X about 6 to about 40 AA residues corresponding in AA residue sequence
 X to an antigenic determinant of HBxAg (see AAP50458-P50460). The
 X antigenic polypeptides may be used in a diagnostic assay system for
 X determining the presence of HBxAg in a body sample.
 X (Updated on 25-MAR-2003 to correct PF field.)
 X (Updated on 25-MAR-2003 to correct PA field.)
 X Q Sequence 154 AA;
 Query Match 100.0%; Score 42; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Y 1 AMSTTDLEA 9
 b 102 AMSTTDLEA 110
 RESULT 10
 AP82174
 D AAP82174 standard; protein; 154 AA.
 X AAP82174;
 I 25-MAR-2003 (updated)
 T 01-JAN-1980 (first entry)
 E Peptide encoded by HBxAg gene.
 X Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;
 X Hepatitis B virus.
 Key Location/Qualifiers
 Region 23..0
 Region /label=Portion of HbxAg expressed by SVBHV-3
 Region 100..115
 Region /label=Synthetic polypeptide 99
 Region 115..131
 Region /label=Synthetic polypeptide 100
 Region 144..154
 Region /label=Synthetic polypeptide 142
 WO8809340-A.
 01-DEC-1988.
 24-MAY-1988; 88WO-US01719.
 26-MAY-1987; 87US-0054424.
 (SCRI) SCRIPPS CLINIC & RES FOUND.
 Moriarty AM;
 WPI; 1988-353925/49.

PT Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 PT corresponding to an antigenic determinant of hepatitis B virus, HBxAg
 XX Disclosure; Fig. 6; 106pp; English.
 PS The polypeptide is encoded by the HbxAg gene.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 154 AA;
 Query Match 100.0%; Score 42; DB 9; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 QY 1 AMSTTDLEA 9
 Db 102 AMSTTDLEA 110
 RESULT 11
 AAY58473
 ID AAY58473 standard; protein; 154 AA.
 XX AC AAY58473;
 XX DT 10-APR-2000 (first entry)
 XX DE Hepatitis B virus (HBV) protein X.
 XX KW HBV protein X; proteasome activity; degradation; virus component;
 KW viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
 KW virucide.
 XX OS Hepatitis b virus.
 XX PN WO9966065-A2.
 XX PD 23-DEC-1999.
 XX PF 10-JUN-1999; 99WO-GB01840.
 XX PR 13-JUN-1998; 98GB-0012756.
 PR 13-JUN-1998; 98GB-0012757.
 PR 13-JUN-1998; 98GB-0012758.
 PR 13-JUN-1998; 98GB-0012759.
 PR 13-JUN-1998; 98GB-0012760.
 XX PA (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
 XX PI Schmid HP, Petit F, Kloetzel PM, Jarrousse AS, Gautier K;
 PI Badaoui S, Mouzeyar S, Nicolas P;
 XX WPI; 2000-106109/09.
 DR Novel assay methods for identifying compounds which modulate and/or
 PT regulate proteasomal activity -
 PT regulate proteasomal activity -
 XX Example 1; Page 8; 35pp; English.
 PS The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteasomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteasomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral
 CC gene product, and protein or peptide substrates; measuring protease
 CC activity; and identifying the compound as an inhibitor if the protease
 CC activity of the assay system is increased. The assays of the invention
 CC can be used to identify compounds which inhibit viral replication and
 CC pathogenesis, and modulate and/or regulate proteasome activity.
 CC Compounds which increase proteasomal degradation of viral components or
 CC molecules induced by viral infection are of value in the treatment of
 CC viral disease. Compounds which modulate proteasomal nuclease activity
 CC have use in the treatment of inflammatory disease, and AIDS in HIV

CC infected patients. The methods may also be used to generate resistance
 CC to bacterial or viral damage. Sequences AAY58472-Y8474 represent
 CC examples of viral proteins which affect proteasomal function.

XX SQ Sequence 154 AA;
 Query Match 100.0%; Score 42; DB 21; Length 154;
 Best Local Similarity 100.0%; Pred. NO. 0.62;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 12

AAV54047
 ID AAY54047 standard; Protein; 154 AA.

XX AC AAY54047;

XX DT 27-MAR-2000 (first entry)

XX DE Amino acid sequence of a HBV transactivating X protein.

XX KW HBV; HBV surface antigen-'S'-133 Oon strain (Met to Thr);
 XX KW DNA polymerase; large surface antigen; core protein;
 XX KW transactivating X protein; hepatitis vaccine; HBV infection;
 XX KW hepatocellular carcinoma.

XX OS Hepatitis B virus.

XX PN WO9966048-A1.

XX PD 23-DEC-1999.

XX PF 19-JUN-1998; 98WO-SG00046.

XX PR 19-JUN-1998; 98WO-SG00046.

XX PA (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

XX PI Oon CJ, Lim GK, Zhao Y, Chen WN;

XX QY WPI; 2000-106104/09.

XX DR N-PSDB; AAZ37088.

XX PT New isolated hepatitis B virus strain, useful for, e.g. treatment of
 XX PT hepatitis infection -

XX PS Disclosure; Page 42; 68pp; English.

XX CC The present sequence is encoded by the genome of an isolated strain of
 XX CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface
 XX CC antigen-'S'-133 Oon strain (Met to Thr). The viral genome is deposited
 XX CC as ECCC accession numbers P97121501, P97121502 and P97121503. The
 XX CC nucleotide sequence was isolated from hepatocellular carcinoma (HCC).
 XX CC The nucleotide sequence encodes four overlapping proteins, which are
 XX CC a DNA polymerase, a large surface antigen, a core protein, and a
 XX CC transactivating X protein. The large surface antigen differs from the
 XX CC wild type sequence in that it contains a Thr at position 133 of the
 XX CC wild type sequence instead of a Met. The proteins are used to produce
 XX CC antibodies. The proteins, polynucleotide and antibodies can be used for
 XX CC detecting the novel HBV strain. The HBV polypeptides can also be used
 XX CC in hepatitis vaccines. The HBV novel strain polypeptides can be used
 XX CC to identify compounds for treating or preventing HBV infection or
 XX CC hepatocellular carcinoma.

XX SQ Sequence 154 AA;

Query Match 100.0%; Score 42; DB 21; Length 154;

Best Local Similarity 100.0%; Pred. NO. 0.62;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 13

AAV44351
 ID AAY44351 standard; Protein; 154 AA.

XX AC AAY44351;

XX DT 14-MAR-2000 (first entry)

XX DE Human hepatitis B virus trans-activating X protein sequence.

XX KW HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;
 XX KW trans-activating X protein; mutant major surface antigen;
 XX KW human hepatitis B viral genome; hepatocellular carcinoma; HBV infection;
 XX KW human hepatitis B virus surface antigen-'S'-145 Singapore strain;

XX OS Human hepatitis B virus.

XX PN WO9966047-A1.

XX PD 23-DEC-1999.

XX PF 19-JUN-1998; 98WO-SG00045.

XX PR 19-JUN-1998; 98WO-SG00045.

XX PA (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

XX PI Oon CJ, Lim GK, Leong AL, Zhao Y, Chen WN;

XX QY WPI; 2000-106103/09.

XX DR N-PSDB; AAZ29453.

XX PT New vaccine-escape mutant of hepatitis B virus and related proteins,
 XX PT nucleic acids and antibodies, useful for diagnosis, prevention and
 XX PT treatment -

XX PS Disclosure; Fig 7; 65pp; English.

XX CC The present sequence is the trans-activating X protein deduced from the
 XX CC mutant human hepatitis B viral genome. This was isolated from a male,
 XX CC 11 year old Singaporean child which had received standard HBIG and HB
 XX CC vaccine and was infected with the mutated strain designated human
 XX CC hepatitis B virus surface antigen-'S'-145 Singapore strain a Year
 XX CC later. This protein can be produced by recombinant technology and used in
 XX CC developing polyclonal or monoclonal antibodies and as a source of
 XX CC diagnostic oligonucleotides. The mutated major surface antigen is used to
 XX CC raise specific antibodies, to identify specific binding agents and, in
 XX CC vaccines or compositions for treatment or prevention of HBV infection and
 XX CC hepatocellular carcinoma. Antibodies are used in diagnosis or for
 XX CC screening donated body fluids or tissues.

XX SQ Sequence 154 AA;

Query Match 100.0%; Score 42; DB 21; Length 154;

Best Local Similarity 100.0%; Pred. NO. 0.62;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMSTTDLEA 9
 |||||
 DB 102 AMSTTDLEA 110

RESULT 14

ABJ07178
 ID ABJ07178 standard; Peptide; 8 AA.

XX

ABJ07178;
 14-NOV-2002 (first entry)
 Hepatitis B virus epitope #1396.
 Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.
 Hepatitis B virus.
 WO200219986-A1.
 14-MAR-2002.
 08-SEP-2000; 2000WO-US24802.
 08-SEP-2000; 2000WO-US24802.
 (EPIM-) EPIMMUNE INC.
 (SETT/) SETTE A.
 Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 Celis E, Kubo RT, Grey HM, Chesnut RW;
 WPI: 2002-643192/69.
 Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -
 Disclosure: Page 137; 228pp; English.
 The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.
 Sequence 8 AA;
 Query Match 90.5%; Score 38; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 MSTTDLEA 9
 |||||
 1 MSTTDLEA 8
 SULT 15
 WO8117
 ABJ08117 standard; Peptide; 8 AA.
 ABJ08117;
 14-NOV-2002 (first entry)
 Hepatitis B virus epitope #2335.
 Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 virucide; hepatotropic; antiinflammatory.
 Hepatitis B virus.
 WO200219986-A1.
 14-MAR-2002.
 08-SEP-2000; 2000WO-US24802.
 08-SEP-2000; 2000WO-US24802.

PA (EPIM-) EPIMMUNE INC.
 PA (SETT/) SETTE A.
 PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX WPI: 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises
 PT a HBV peptide epitope -
 XX Disclosure: Page 160; 228pp; English.
 PS The present invention relates to a composition comprising at least one
 XX hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 90.5%; Score 38; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTTDLEA 9
 |||||
 Db 1 MSTTDLEA 8

Search completed: December 23, 2003, 08:44:01
 Job time : 26.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 08:39:57 ; Search time 25.8 Seconds
(without alignments)
55.370 Million cell updates/sec

Title: US-09-989-621-5

Perfect score: 41

Sequence: 1 EIRLKVFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_19Jun03.*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	9	14 AAR33297	Cytotoxic T-lymphocyte
2	41	100.0	9	20 AAR52983	Hepatitis B virus
3	41	100.0	9	20 AAY24463	Hepatitis B virus
4	41	100.0	15	23 ABJ08326	Hepatitis B virus
5	41	100.0	15	23 ABJ08326	Hepatitis B virus
6	41	100.0	24	11 AAR07458	Peptide immunoreac
7	41	100.0	24	11 AAR07460	Peptide immunoreac
8	41	100.0	37	17 AAR94599	X-protein peptide.
9	41	100.0	154	6 AAP50461	Sequence of the an

10	41	100.0	154	9 AAP82174	Peptide encoded by
11	41	100.0	154	21 AAY58473	Hepatitis B virus
12	40	97.6	154	21 AAY44351	Human hepatitis B
13	37	90.2	154	21 AAY54047	Amino acid sequenc
14	36	87.8	424	22 AAY33217	Novel human secret
15	34	82.9	24	11 AAR07459	Peptide immunoreac
16	34	82.9	476	19 AAW15337	Helicobacter polyp
17	32	78.0	11	23 ABJ06460	Hepatitis B virus
18	32	78.0	11	23 ABJ08203	Hepatitis B virus
19	32	78.0	11	23 ABJ08526	Hepatitis B virus
20	32	78.0	73	22 ABG39682	Novel human diagno
21	31	75.6	230	18 AAW32421	Mycobacterium tube
22	31	75.6	230	18 AAW32353	Mycobacterium tube
23	31	75.6	230	19 AAW81656	M. tuberculosis in
24	31	75.6	230	19 AAW64293	Mycobacterium tube
25	31	75.6	230	20 AAY39095	M. tuberculosis an
26	31	75.6	230	20 AAY38958	M. tuberculosis re
27	31	75.6	560	22 ABB71498	Drosophila melanog
28	30	73.2	80	23 ABJ05388	Carp acyl coenzyme
29	30	73.2	83	22 AAM40407	Human polyptide
30	30	73.2	110	22 AAG66775	Human ribosomal S1
31	30	73.2	126	22 AAM25829	Human protein sequ
32	30	73.2	126	22 AAM42193	Human polyptide
33	29	70.7	39	22 AAU23594	Novel human enzyme
34	29	70.7	60	22 ABG02407	Novel human diagno
35	29	70.7	68	22 AAY34372	Human reproductive
36	29	70.7	93	22 ABG02405	Novel human diagno
37	29	70.7	107	21 AAG02404	Human secreted pro
38	29	70.7	134	16 AAR71563	Hepatitis B virus
39	29	70.7	164	22 ABG02409	Novel human diagno
40	29	70.7	216	20 AAY19974	B. burgdorferi ant
41	29	70.7	228	16 AAR71113	Mycobacterial prot
42	29	70.7	228	18 AAW18181	Mycobacterium tube
43	29	70.7	228	19 AAM63036	Mycobacterium tube
44	29	70.7	228	23 AAM50742	Mycobacterium tube
45	29	70.7	284	24 ABP75887	Human secretory po

ALIGNMENTS

RESULT 1
AAR33297
ID AAR33297 standard; peptide; 9 AA.
AC AAR33297;
XX
DT 25-MAR-2003 (updated)
DT 02-JUL-1993 (first entry)
XX
Cytotoxic T-lymphocyte inducing peptide HBP01126-134.
DE
KW MHC class I; major histocompatibility complex class I; CTL-response;
KW HBV; hepatitis B virus; vaccine; treatment; T-helper cell mediated.
XX
OS Synthetic.
XX
PN WO9303753-A1.
XX
PD 04-MAR-1993.
XX
PF 26-AUG-1992; 92WO-US07213.
XX
PR 26-AUG-1991; 91US-0749540.
XX
PA (SCRI) SCRIpps RES INST.
XX
PI Chisari FV, Ferrari C, Missale G, Penna A;
DR WPI, 1993-093719/11.
XX
PT Cytotoxic T-lymphocyte-inducing peptide(s) from hepatitis B virus
- for preventing and treating virus infections, and identifying

PT individuals susceptible to developing chronic virus infection

PS Claim 18; Page 11; 76pp; English.

CC This peptide induces MHC class I restricted CTL responses against
 CC HBV (pref. restricted to HLA-A2, HLA31 or HLA-Aw68). It can be used
 CC for treating HBV infection, in vaccines against HBV, or may be
 CC joined to a second immunogenic peptide to elicit a T-helper cell
 CC mediated response.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 1 EIRLKVFL 9

RESULT 2

AAW52983
 ID AAW52983 standard; peptide; 9 AA.

AC AAW52983;

DT 12-MAR-2002 (first entry)

DE Hepatitis B virus X protein peptide (residues 126-134).

KW HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I;
 KW major histocompatibility complex; immunomodulator.

OS Hepatitis B virus.

PN KR98022440-A.

PD 06-JUL-1998.

PF 23-SEP-1996; 96KR-0041612.

PR 23-SEP-1996; 96KR-0041612.

PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.

PI Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;

XX WPI; 1999-300977/25.

PT Synthetic peptide having immunoregulating activities for hepatitis B
 PT virus -

PS Example 1; Page 4; 7pp; Korean.

CC The invention relates to peptides derived from the hepatitis B virus
 CC (HBV) X protein (AAW52970-AAW52973). The peptides are presented on major
 CC histocompatibility complex (MHC) class I molecules and act as cytotoxic
 CC T-lymphocyte (CTL) epitopes. Sequences AAW52974-AAW52984 represent HBV
 CC X protein-derived peptides used in an exemplification of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 1 EIRLKVFL 9

RESULT 3

AAW24463
 ID AAW24463 standard; peptide; 9 AA.

AC AAW24463;

DT 23-SEP-1999 (first entry)

DE Hepatitis B virus X protein peptide #5.

KW Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;
 KW CTL; antigen; immunity; liver cancer.

OS Hepatitis B virus.

OS Synthetic.

PN WO9936434-A1.

PD 22-JUL-1999.

XX 19-JAN-1998; 98WO-KR00010.

XX 19-JAN-1998; 98WO-KR00010.

PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

PI Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;

PI Lee K;

DR WPI; 1999-444387/37.

PT Hepatitis B virus protein X-derived peptide antigens used to
 PT stimulate cytotoxic T lymphocytes, useful for treatment of
 PT HBV-associated diseases, especially liver cancer

XX Claim 5; Page 24; 33pp; English.

CC The present invention describes peptide antigens AAW24459 to AAW24463
 CC derived from the X protein of hepatitis B virus (HBV) which are
 CC recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CC derived from HBV X protein are useful for inducing CTLs against the
 CC virus or inducing immunological tolerance to the virus. pH-sensitive
 CC liposomes containing the peptide antigens are used to induce cellular
 CC immunity so that CTLs specific to the virus can be produced. This is
 CC useful for prevention and treatment of HBV-associated diseases,
 CC especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CC the selective transportation of anti-cancer drugs.

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9

Db 1 EIRLKVFL 9

RESULT 4

ABJ08926
 ID ABJ08926 standard; Peptide; 15 AA.

AC ABJ08926;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #3144.

KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

CX WO200219986-A1.
 CX 14-MAR-2002.
 CX 08-SEP-2000; 2000WO-US24802.
 CX 08-SEP-2000; 2000WO-US24802.
 CX (EPIM-) EPIMUNE INC.
 CX (SETT/) SETTE A.
 CX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 CX Celis E, Kubo RT, Grey HM, Chesnut RW;
 CX WPI; 2002-643192/69.
 CX Vaccine composition for treating or preventing hepatitis B virus (HBV)
 CX infection, and/or for stimulating an immune response to HBV, comprises
 CX a HBV peptide epitope -
 CX Disclosure; Page 179; 228pp; English.
 CX The present invention relates to a composition comprising at least one
 CX hepatitis B virus epitope. This can be used in the production of a
 CX vaccine for use in preventing or treating hepatitis B virus infection.
 CX The present sequence is a peptide described in the exemplification of the
 CX invention.
 CX Sequence 15 AA;
 CX Query Match 100.0%; Score 41; DB 23; Length 15;
 CX Best Local Similarity 100.0%; Pred. No. 0.016;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX 1 EIRLKVFL 9
 CX |||||
 CX 1 EIRLKVFL 9
 CX
 CX RESULT 5
 CX ABJ09218
 CX ID ABJ09218 standard; Peptide; 15 AA.
 CX AC ABJ09218;
 CX 14-NOV-2002 (first entry)
 CX Hepatitis B virus epitope #3436.
 CX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 CX virucide; hepatotropic; antiinflammatory.
 CX Hepatitis B virus.
 CX WO200219986-A1.
 CX 14-MAR-2002.
 CX 08-SEP-2000; 2000WO-US24802.
 CX 08-SEP-2000; 2000WO-US24802.
 CX (EPIM-) EPIMUNE INC.
 CX (SETT/) SETTE A.
 CX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 CX Celis E, Kubo RT, Grey HM, Chesnut RW;
 CX WPI; 2002-643192/69.
 CX Vaccine composition for treating or preventing hepatitis B virus (HBV)
 CX infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -
 XX Disclosure; Page 182; 228pp; English.
 XX
 XX The present invention relates to a composition comprising at least one
 XX hepatitis B virus epitope. This can be used in the production of a
 XX vaccine for use in preventing or treating hepatitis B virus infection.
 XX The present sequence is a peptide described in the exemplification of the
 XX invention.
 XX Sequence 15 AA;
 XX Query Match 100.0%; Score 41; DB 23; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 0.016;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 EIRLKVFL 9
 XX |||||
 XX 1 EIRLKVFL 9
 XX
 XX RESULT 6
 XX AAR07458
 XX ID AAR07458 standard; peptide; 24 AA.
 XX AC AAR07458;
 XX 25-MAR-2003 (updated)
 XX 04-FEB-1991 (first entry)
 XX Peptide immunoreactive with hepatitis B antibody (I).
 XX Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 XX immunoassay; chronic hepatitis.
 XX Synthetic.
 XX DB4011768-A.
 XX 18-OCT-1990.
 XX 11-APR-1990; 90DE-4011768.
 XX 14-APR-1989; 89JP-0095015.
 XX (OLYU) OLYMPUS OPTICAL CO LTD.
 XX Kumazawa T, Otsu M;
 XX WPI; 1990-321759/43.
 XX New polypeptide deriva. immune reactive with hepatitis B antibody
 XX - useful as immunoassay reagents, e.g. for diagnosing
 XX hepatocellular carcinoma
 XX Claim 1; Page 8; 13pp; German.
 XX The peptide corresp. to a partic. fragment (amino acids 114-137) of
 XX the sequence encoded by the X-gene of HBV adr subtype. When
 XX immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 XX etc., the peptides are useful as immunoassay reagents, for detecting
 XX Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 XX hepatitis. They can also be used as immunogens to raise antibodies.
 XX See also AAR07458-60.
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 24 AA;
 XX Query Match 100.0%; Score 41; DB 11; Length 24;
 XX Best Local Similarity 100.0%; Pred. No. 0.027;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 EIRLKVFL 9

KW X-protein; hepatitis B virus; Kunitz domain; transactivation;
KW site-directed mutagenesis; proteasome complex subunit; human;
KW XAPC7; S4; therapy; diagnostic; antigen; antibody; immunoassay;

X

PR 13-JUN-1998; 98GB-0012759.
 PR 13-JUN-1998; 98GB-0012760.

XX (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.

PA Schmid HP, Petit F, Kloetzel PM, Jarrousse AS, Gautier K;
 PI Badaoui S, Mouzeyar S, Nicolas P;
 XX WPI; 2000-106109/09.

DR WPI; 2000-106109/09.

XX Novel assay methods for identifying compounds which modulate and/or
 PT regulate proteasomal activity -
 XX Example 1; Page 8; 35pp; English.

XX The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteasomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteasomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral
 CC gene product, and protein or peptide substrates, measuring protease
 CC activity; and identifying the compound as an inhibitor if the protease
 CC activity of the assay system is increased. The assays of the invention
 CC can be used to identify compounds which inhibit viral replication and
 CC pathogenesis, and modulate and/or regulate proteasome activity.
 CC Compounds which increase proteasomal degradation of viral components or
 CC molecules induced by viral infection are of value in the treatment of
 CC viral disease. Compounds which modulate proteasomal nuclease activity
 CC have use in the treatment of inflammatory disease, and AIDS in HIV
 CC infected patients. The methods may also be used to generate resistance
 CC to bacterial or viral damage. Sequences AAY58472-Y58474 represent
 CC examples of viral proteins which affect proteasomal function.

XX Sequence 154 AA;

Query Match 100.0%; Score 41; DB 21; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
 DB 126 EIRLKVFL 134

RESULT 12

AY44351
 ID AAY44351 standard; Protein; 154 AA.

XX AY44351;

DT 14-MAR-2000 (first entry)

XX Human hepatitis B virus trans-activating X protein sequence.

XX HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;
 KW trans-activating X protein; mutant major surface antigen;
 KW human hepatitis B viral genome; hepatocellular carcinoma; HBV infection;
 KW human hepatitis B virus surface antigen- 'S' - 145 Singapore strain;
 OS Human hepatitis B virus.

XX WO9966047-A1.

XX 23-DEC-1999.

XX 19-JUN-1998; 98WO-SG00045.

XX 19-JUN-1998; 98WO-SG00045.

XX (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 PA Con CU, Lim GK, Leong AL, Zhao Y, Chen WN;

XX WPI; 2000-106104/09.

XX N-PSDB; AAZ37088.

XX New isolated hepatitis B virus strain, useful for, e.g. treatment of
 PT hepatitis infection -
 XX Disclosure; Page 42; 68pp; English.

XX The present sequence is encoded by the genome of an isolated strain of
 CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface

XX WPI; 2000-106103/09.
 DR N-PSDB; AAZ29453.

XX New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment -
 XX Disclosure; Fig 7; 65pp; English.

XX The present sequence is the trans-activating X protein deduced from the
 CC mutant human hepatitis B viral genome. This was isolated from a male,
 CC 11 year old Singaporean child which had received standard HBIG and HB
 CC vaccine and was infected with the mutated strain designated human
 CC hepatitis B virus surface antigen- 'S' - 145 Singapore strain a year
 CC later. This protein can be produced by recombinant technology and used in
 CC developing polyclonal or monoclonal antibodies and as a source of
 CC diagnostic oligonucleotides. The mutated major surface antigen is used to
 CC raise specific antibodies, to identify specific binding agents and, in
 CC vaccines or compositions for treatment or prevention of HBV infection and
 CC hepatocellular carcinoma. Antibodies are used in diagnosis or for
 CC screening donated body fluids or tissues.

XX Sequence 154 AA;

Query Match 97.6%; Score 40; DB 21; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.35;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKVFL 9
 DB 126 EIRLKVFL 134

RESULT 13

AY54047
 ID AAY54047 standard; Protein; 154 AA.

XX AY54047;

DT 27-MAR-2000 (first entry)

XX Amino acid sequence of a HBV transactivating X protein.

XX HBV; HBV surface antigen- 'S' - 133 Oon strain (Met to Thr);
 KW DNA polymerase; large surface antigen; core protein;
 KW transactivating X protein; hepatitis vaccine; HBV infection;
 KW hepatocellular carcinoma.

XX Hepatitis B virus.

XX WO9966048-A1.

XX 23-DEC-1999.

XX 19-JUN-1998; 98WO-SG00046.

XX 19-JUN-1998; 98WO-SG00046.

XX (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 PA Con CU, Lim GK, Zhao Y, Chen WN;

XX WPI; 2000-106104/09.

XX N-PSDB; AAZ37088.

XX New isolated hepatitis B virus strain, useful for, e.g. treatment of
 PT hepatitis infection -
 XX Disclosure; Page 42; 68pp; English.

XX The present sequence is encoded by the genome of an isolated strain of
 CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface

CC antigen-'S'-133 Con strain (Wet to Thr). The viral genome is deposited
 CC as ECCC accession numbers P97121501, P97121502 and P97121503. The
 CC nucleotide sequence was isolated from hepatocellular carcinoma (HCC).
 CC The nucleotide sequence encodes four overlapping proteins, which are
 CC a DNA polymerase, a large surface antigen, a core protein, and a
 CC transactivating X protein. The large surface antigen differs from the
 CC wild type sequence in that it contains a Thr at position 133 of the
 CC wild type sequence instead of a Met. The proteins are used to produce
 CC antibodies. The proteins, polynucleotide and antibodies can be used for
 CC detecting the novel HBV strain. The HBV polypeptides can also be used
 CC in hepatitis vaccines. The HBV novel strain polypeptides can be used
 CC to identify compounds for treating or preventing HBV infection or
 CC hepatocellular carcinoma.

Q Sequence 154 AA;
 Query Match 90.2%; Score 37; DB 21; Length 154;
 Best Local Similarity 77.8%; Pred. No. 1.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 EIRLKVFL 9
 126 EIRLKIYVL 134

RESULT 14
 AU33217
 D AAU33217 standard; Protein; 424 AA.
 C AAU33217;
 T 18-DEC-2001 (first entry)
 X Homo sapiens.
 E Novel human secreted protein #3708.
 W Human; vaccination; gene therapy; nutritional supplement;
 W stem cell proliferation; hematopoiesis; nerve tissue regeneration;
 W immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 S WO200179449-A2.
 N 25-OCT-2001.
 D 16-APR-2001; 2001WO-US08656.
 F 18-APR-2000; 2000US-0552929.
 R 26-JAN-2001; 2001US-0770160.
 R (HYSE-) HYSEQ INC.
 A Tang YT, Liu C, Drmanac RT;
 I WPI; 2001-611725/70.
 X Nucleic acids encoding a range of human polypeptides, useful in genetic
 T vaccination, testing and therapy -
 K Claim 20; Page 733; 765pp; English.

The invention relates to novel human secreted polypeptides. The
 S polypeptides and antibodies to the polypeptides are useful for
 S determining the presence of or predisposition to a disease associated
 S with altered levels of polypeptide. The polypeptides are also useful for
 S identifying agents (agonists and antagonists) that bind to them. Cells
 S expressing the proteins are useful for identifying a therapeutic agent
 S for use in treatment of a pathology related to aberrant expression or
 S physiological interactions of the polypeptide. Vectors comprising
 S the nucleic acids encoding the polypeptides and cells genetically
 S engineered to express them are also useful for producing the proteins.
 S The proteins are useful in genetic vaccination, testing and
 S therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

Q Sequence 424 AA;
 Query Match 87.8%; Score 36; DB 22; Length 424;
 Best Local Similarity 87.5%; Pred. No. 8.6;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKVFL 8
 250 EVRLKVFV 257

Db 250 EVRLKVFV 257

RESULT 15
 AAR07459
 ID AAR07459 standard; protein; 24 AA.
 X AAR07459;
 AC 25-MAR-2003 (updated)
 XX 04-FEB-1991 (first entry)
 DT Peptide immunoreactive with hepatitis B antibody (II).
 DT Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 XX immunocassay; chronic hepatitis.
 XX Synthetic.
 XX DB4011768-A.
 PN 18-OCT-1990.
 XX 11-APR-1990; 90DB-4011768.
 PF 14-APR-1989; 89JP-0095015.
 XX (OLYU) OLYMPUS OPTICAL CO LTD.
 PA Kumazawa T, Osanai M;
 PI WPI; 1990-321759/43.
 XX New polypeptide derivs. immune reactive with hepatitis B antibody
 PT - useful as immunoassay reagents, e.g. for diagnosing
 PT hepato:cellular carcinoma
 XX Claim 3; Page 8; 13pp; German.
 PS The peptide corresp. to a partic. fragment (amino acids 114-137) of
 CC the sequence encoded by the X-gene of HBV adw subtype. When
 CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 CC etc., the peptides are useful as immunoassay reagents for detecting
 CC Abs. esp. for diagnosis of hepatocellular carcinoma and chronic
 CC hepatitis. They can also be used as immunogens to raise antibodies.
 CC See also AAR07458-60.
 CC (Updated on 25-MAR-2003 to correct PA field.)

Q Sequence 24 AA;
 Query Match 82.9%; Score 34; DB 11; Length 24;
 Best Local Similarity 77.8%; Pred. No. 1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLKVFL 9
 13 EIRLMIFVL 21

Db 13 EIRLMIFVL 21

Search completed: December 23, 2003, 08:44:04
Job time : 26.8 secs

PI Grey HM, Kast WM, Sette A, Sidney J;

Best Local Similarity	100.0%;	Pred. No.	9.3e+05;	Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	CLFKDWEEL	9										
DB	1	CLFKDWEEL	9										
RESULT 3													
AAY24462													
ID	AAY24462 standard; peptide; 9 AA.												
XX	XX	AC	AC										
XX	AAY24462;												
DT	23-SEP-1999 (first entry)												
XX	XX	Hepatitis B virus X protein peptide #4.											
XX	XX	Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;											
KW	KW	CTL; antigen; immunity; liver cancer.											
KW	KW												
OS	OS	Hepatitis B virus.											
OS	OS	Synthetic.											
XX	XX												
PN	PN	WO9936434-A1.											
XX	XX												
PD	PD	22-JUL-1999.											
XX	XX												
PF	PF	19-JAN-1998; 98WO-KR00010.											
XX	XX												
PR	PR	19-JAN-1998; 98WO-KR00010.											
XX	XX												
PA	PA	(MOGA-) MOGAM BIOTECHNOLOGY RES INST.											
XX	XX												
PI	PI	Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;											
PI	PI	Lee K;											
XX	XX												
DR	DR	WPI; 1999-444387/37.											
XX	XX												
PT	PT	Hepatitis B virus protein X-derived peptide antigens used to											
PT	PT	stimulate cytotoxic T lymphocytes, useful for treatment of											
PT	PT	HBV-associated diseases, especially liver cancer											
XX	XX												
PS	PS	Claim 4; Page 24; 33pp; English.											
XX	XX												
CC	CC	The present invention describes peptide antigens AAY24459 to AAY24463											
CC	CC	derived from the X protein of hepatitis B virus (HBV) which are											
CC	CC	recognized by cytotoxic T lymphocytes (CTL). The peptide antigens											
CC	CC	derived from HBV X protein are useful for inducing CTLs against the											
CC	CC	virus or inducing immunological tolerance to the virus. pH-sensitive											
CC	CC	liposomes containing the peptide antigens are used to induce cellular											
CC	CC	immunity so that CTLs specific to the virus can be produced. This is											
CC	CC	useful for prevention and treatment of HBV-associated diseases,											
CC	CC	especially HBV-associated liver cancer. pH-sensitive liposomes permit											
CC	CC	the selective transportation of anti-cancer drugs.											
XX	XX												
SQ	SQ	Sequence 9 AA;											
Query Match 100.0%; Score 55; DB 20; Length 9;													
Best Local Similarity	100.0%;	Pred. No.	9.3e+05;	Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	CLFKDWEEL	9										
DB	1	CLFKDWEEL	9										
RESULT 4													
AAP82169													
ID	AAP82169 standard; protein; 18 AA.												
XX	XX												
AC	AC	AAP82169;											
XX	XX												

25-MAR-2003 (updated)
 06-JAN-1991 (first entry)
 Antigenic determinant of HBxAg.
 Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;
 Hepatitis B virus.
 WO8809340-A.
 01-DEC-1988.
 24-MAY-1988; 85WO-US01719.
 26-MAY-1987; 87US-0054424.
 (SCHI) SCRIPPS CLINIC & RES FOUND.
 Moriarty AM;
 WPI; 1988-353925/49.
 Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 corresponding to an antigenic determinant of hepatitis B virus, HBxAg
 Claim 4; Page 90; 106pp; English.
 The peptide and antibodies reactive with it are used in diagnostic
 assays for HBxAg in a body sample. They can also be used in affinity
 matrices for isolation and purification.
 (Updated on 25-MAR-2003 to correct PA field.)
 Sequence 18 AA;
 Query Match 100.0%; Score 55; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CLFKDWEEL 9
 |||||
 1 CLFKDWEEL 9

SULT 5
 207460
 AAR07460 standard; protein; 24 AA.
 AAR07460;
 25-MAR-2003 (updated)
 04-FEB-1991 (first entry)
 Peptide immunoreactive with hepatitis B antibody (III).
 Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 immunoassay; chronic hepatitis.
 Synthetic.
 DE4011768-A.
 18-OCT-1990.
 11-APR-1990; 90DE-4011768.
 14-APR-1989; 89JP-0095015.
 (OLYU) OLYMPUS OPTICAL CO LTD.
 Kumazawa T, Oeana M;
 WPI; 1990-321759/43.

XX New polypeptide derivs. immune reactive with hepatitis B antibody
 PT - useful as immunoassay reagents, e.g. for diagnosing
 PT hepato:cellular carcinoma
 XX
 PS Claim 4; Page 8; 13pp; German.
 XX
 CC The peptide corresp. to a partic. fragment (amino acids 114-137) of
 CC the sequence encoded by the X-gene of HBV avr subtype. When
 CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 CC etc., the peptides are useful as immunoassay reagents for detecting
 CC Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 CC hepatitis. They can also be used as immunogens to raise antibodies.
 CC See also AAR07458-60.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 55; DB 11; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLFKDWEEL 9
 |||||
 DB 2 CLFKDWEEL 10

RESULT 6
 AAR94599
 ID AAR94599 standard; Peptide; 37 AA.
 XX
 AC AAR94599;
 XX
 DT 13-JUL-1996 (first entry)
 XX
 DE X-protein peptide.
 KW X-protein; hepatitis B virus; Kunitz domain; transactivation;
 KW site-directed mutagenesis; proteasome complex subunit; human;
 KW XAPC7; S4; therapy; diagnostic; antigen; antibody; immunoassay;
 KW probe; primer.
 XX
 OS Hepatitis B virus.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 10 /note= "Altered to Arg in mutant"
 FT Misc-difference 22 /note= "Altered to Tyr in mutant"
 FT Domain 22..35 /note= "Putative Kunitz domain"
 FT Misc-difference 26 /note= "Altered to Val in mutant"
 FT Misc-difference 27 /note= "Altered to Ser in mutant"
 FT Misc-difference 28 /note= "Altered to Gln in mutant"
 FT Misc-difference 29 /note= "Altered to Asp in mutant"
 XX
 PN WO9611207-A1.
 XX
 PD 18-APR-1996.
 XX
 PF 05-OCT-1995; 95WO-US13426.
 XX
 PR 06-OCT-1994; 94US-0319376.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Huang J, Liang TJ;
 XX
 DR WPI; 1996-209804/21.

X Prevention of interaction of HBV X and XAPC7 or S4 protein - using
T a peptide which interferes with HBV infection, useful in treatment
R of HBV infection
K

Claim 10; Fig 4; 45pp; English.

The sequence represents a fragment (amino acids 111-147) of hepatitis B virus (HBV) X-protein (HBX), containing a putative Kunitz domain, which is crucial for transactivation function of HBX. Key residues in this domain have been mutated and transactivation properties of mutants have been studied. HBX has been identified as interacting with human proteasome complex subunits XAPC7 (C7, AAR94597) and S4 (AAR94600). Mutagenesis of critical residues has shown that this 2nd domain is important for interaction with C7, and this phenotype shows a close association with transactivation activity. Peptides derived from the HBX protein may be used to interact with proteasome subunits and interfere with HBV infection, and are thus useful in therapy of hepatitis B. Such peptides are also useful as antigens to generate polyclonal or monoclonal antibodies for diagnostic applications. DNA probes and primers based on the sequence may also be used to detect HBV infection.

Sequence 37 AA;

Query Match 100.0%; Score 55; DB 17; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9
|||||||
5 CLFKDWEEL 13

RESULT 7
AAR71563
AAR71563 standard; Protein; 134 AA.

AAR71563;

01-NOV-1995 (first entry)

Hepatitis B virus polypeptide.

Hepatitis B virus; PCR; amplification; primer; antiviral agent.

Hepatitis B virus.

JP07033797-A.

03-FEB-1995.

21-JUL-1993; 93JP-0180314.

21-JUL-1993; 93JP-0180314.

(MITU) MITSUBISHI KASEI CORP.

WPI; 1995-110649/15.

N-PSDB; AAR85966.

Polypeptide derived from hepatitis B virus and its coding gene.
- may be used for detection of HBV not detectable by conventional methods

Claim 1; Page 6; 7pp; Japanese.

The amino acid sequence of a polypeptide derived from hepatitis B virus. The gene encoding this protein was derived from DNA isolated from patients infected with hepatitis virus which was not detected by conventional methods. The fragment encoding the polypeptide was subsequently PCR amplified using primers (AAR85967-70). The polypeptide can be used in the diagnosis of hepatitis viral diseases which cannot be

CC detected by conventional methods and in the development of antiviral
agents.

XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 55; DB 16; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9

|||||||
115 CLFKDWEEL 123

RESULT 8

AAP50461

ID AAP50461 standard; protein; 154 AA.

XX AAP50461;

XX 25-MAR-2003 (updated)

DT 27-SEP-1991 (first entry)

DE Sequence of the antigen HBxAg encoded by the X region of the
hepatitis B virus genome.

KW Hepatitis B virus; X region; antigen; diagnostic assay.

OS Hepatitis B virus.

FT Key Location/Qualifiers

FT Region 23..154

FT /note= "the substantial portion of HBxAg expressed
by SVBHV-3. Ala (23) is the amino-terminal
residue of the expressed HBxAg polypeptide"

FT Peptide 100..115

FT /label= Peptide 99

FT Peptide 115..131

FT /label= Peptide 100

FT Peptide 144..154

FT /label= Peptide 142

XX W08503950-A.

XX 12-SEP-1985.

XX 06-MAR-1985; 85WO-US00359.

XX 07-SEP-1984; 84US-0648142.

XX 08-MAR-1984; 84US-0587570.

XX 26-MAY-1987; 87US-0054424.

XX (SCRI) SCRIPPS CLINIC & RES FOUND.

XX Moriarty AM, Alexander H, Lerner RA;

XX WPI; 1985-236420/38.

XX Expression vector contg. gene coding for hepatitis B HBxAg -

XX useful in diagnostic systems for detection of HBxAg and its

XX antibody in body samples

XX Disclosure; Fig 6; 86pp; English.

XX The inventors claim an antigenic synthetic polypeptide containing

XX about 6 to about 40 AA residues corresponding in AA residue sequence

XX to an antigenic determinant of HBxAg (see AAP50458-P50460). The

XX antigenic polypeptides may be used in a diagnostic assay system for

XX determining the presence of HBxAg in a body sample.

XX (Updated on 25-MAR-2003 to correct Pr field.)

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 154 AA;

Query Match 100.0%; Score 55; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9
 |||||
 115 CLFKDWEEL 123

SULT 9
 82174

AAP82174 standard; protein; 154 AA.

AAP82174;

25-MAR-2003 (updated)
 01-JAN-1980 (first entry)

Peptide encoded by HBxAg gene.

Antigenic peptide; HBxAg; antigenic polymer; assay; diagnosis;

Hepatitis B virus.

Key Location/Qualifiers
 Region 23..0
 /label=Portion of HBxAg expressed by SVBHV-3
 Region 100..115
 /label=Synthetic polypeptide 99
 Region 115..131
 /label=Synthetic polypeptide 100
 Region 144..154
 /label=Synthetic polypeptide 142

W08809340-A.

01-DEC-1988.

24-MAY-1988; 88WO-US01719.

26-MAY-1987; 87US-0054424.

(SCRI) SCRIPPS CLINIC & RES FOUND.

Moriarty AM;

WPI; 1988-353925/49.

Antigenic synthetic polypeptide(s) - contg. an amino acid sequence
 corresponding to an antigenic determinant of hepatitis B virus, HBxAg

Disclosure; Fig. 6; 106pp; English.

The polypeptide is encoded by the HBxAg gene.
 (Updated on 25-MAR-2003 to correct PA field.)

Sequence 154 AA;

Query Match 100.0%; Score 55; DB 9; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9
 |||||
 115 CLFKDWEEL 123

SULT 10
 07458

AAR07458 standard; peptide; 24 AA.

AAR07458;

XX 25-MAR-2003 (updated)
 DT 04-FEB-1991 (first entry)
 XX Peptide immunoreactive with hepatitis B antibody (I).
 XX Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 KW immunocassay; chronic hepatitis.
 XX Synthetic.
 XX DE4011768-A.
 XX 18-OCT-1990.
 XX 11-APR-1990; 90DE-4011768.
 XX 14-APR-1989; 89JP-0095015.
 XX (OLYU) OLYMPUS OPTICAL CO LTD.
 XX Kumazawa T, Osanai M;
 XX WPI; 1990-321759/43.
 XX New polypeptide derivs. immune reactive with hepatitis B antibody
 PT - useful as immunoassay reagents, e.g. for diagnosing
 PT hepato:cellular carcinoma
 XX Claim 1; Page 8; 13pp; German.
 XX The peptide corresp. to a partic. fragment (amino acids 114-137) of
 CC the sequence encoded by the X-gene of HBV adr subtype. When
 CC immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 CC etc., the peptides are useful as immunoassay reagents, for detecting
 CC Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 CC hepatitis. They can also be used as immunogens to raise antibodies.
 CC See also AAR07458-60.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 24 AA;

Query Match 94.5%; Score 52; DB 11; Length 24;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CLFKDWEEL 9
 |||||
 Db 2 CVFKDWEEL 10

RESULT 11

AAR07459
 ID AAR07459 standard; protein; 24 AA.

XX AAR07459;

XX 25-MAR-2003 (updated)

DT 04-FEB-1991 (first entry)

DE Peptide immunoreactive with hepatitis B antibody (II).

XX Hepatitis B antibody; diagnosis; hepatocellular carcinoma;
 KW immunocassay; chronic hepatitis.

XX Synthetic.

XX DE4011768-A.

XX 18-OCT-1990.

XX 11-APR-1990; 90DE-4011768.

XX

14-APR-1989; 89JP-0095015.
 (OLYU) OLYMPUS OPTICAL CO LTD.
 Kumazawa T, Osanai M;
 WPI; 1990-321759/43.
 New polypeptide derivs. immune reactive with hepatitis B antibody
 - useful as immunoassay reagents, e.g. for diagnosing
 hepato:cellular carcinoma
 Claim 3; Page 8; 13pp; German.
 The peptide corresp. to a partic. fragment (amino acids 114-137) of
 the sequence encoded by the X-gene of HBV adw subtype. When
 immobilised on a carrier, e.g. BSA, latex, microtitre plate wells,
 etc., the peptides are useful as immunoassay reagents, for detecting
 Abs, esp. for diagnosis of hepatocellular carcinoma and chronic
 hepatitis. They can also be used as immunogens to raise antibodies.
 See also AAR07458-60.
 (Updated on 25-MAR-2003 to correct PA field.)
 Sequence 24 AA;
 Query Match 94.5%; Score 52; DB 11; Length 24;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 CLFKDWEEL 9
 :|||||
 2 CVFKDWEEL 10
 RESULT 12
 AAY58473
 AAY58473 standard; protein; 154 AA.
 AAY58473;
 10-APR-2000 (first entry)
 Hepatitis B virus (HBV) protein X.
 HBV protein X; proteasome activity; degradation; virus component;
 viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
 virucide.
 Hepatitis b virus.
 WO9966065-A2.
 23-DEC-1999.
 10-JUN-1999; 99WO-GB01840.
 13-JUN-1998; 98GB-0012756.
 13-JUN-1998; 98GB-0012757.
 13-JUN-1998; 98GB-0012758.
 13-JUN-1998; 98GB-0012759.
 13-JUN-1998; 98GB-0012760.
 (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
 Schmid HP, Petit F, Kloetzel PM, Jarrousse AS, Gautier K;
 Badaoui S, Mouzeyar S, Nicolas P;
 WPI; 2000-106109/09.
 Novel assay methods for identifying compounds which modulate and/or
 regulate proteasomal activity -
 Example 1; Page 8; 35pp; English.

XX The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteasomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteasomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral
 CC gene product, and protein or peptide substrates; measuring protease
 CC activity; and identifying the compound as an inhibitor if the protease
 CC activity of the assay system is increased. The assays of the invention
 CC can be used to identify compounds which inhibit viral replication and
 CC pathogenesis, and modulate and/or regulate proteasome activity.
 CC Compounds which increase proteasomal degradation of viral components or
 CC molecules induced by viral infection are of value in the treatment of
 CC viral disease. Compounds which modulate proteasomal nuclease activity
 CC have use in the treatment of inflammatory disease, and AIDS in HIV
 CC infected patients. The methods may also be used to generate resistance
 CC to bacterial or viral damage. Sequences AAY58472-Y58474 represent
 CC examples of viral proteins which affect proteasomal function.
 XX Sequence 154 AA;
 SQ

Query Match 94.5%; Score 52; DB 21; Length 154;
 Best Local Similarity 88.9%; Pred. No. 0.75;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLFKDWEEL 9
 :|||||
 DB 115 CVFKDWEEL 123

RESULT 13
 AAY54047
 ID AAY54047 standard; Protein; 154 AA.
 XX AAY54047;
 AC AAY54047;
 XX 27-MAR-2000 (first entry)
 DT Amino acid sequence of a HBV transactivating X protein.
 XX
 DE HBV; HBV surface antigen-S'-133 Oon strain (Met to Thr);
 KW DNA polymerase; large surface antigen; core protein;
 KW transactivating X protein; hepatitis vaccine; HBV infection;
 KW hepatocellular carcinoma.
 XX Hepatitis B virus.
 OS
 XX WO9966048-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 19-JUN-1998; 98WO-SG000046.
 XX
 PR 19-JUN-1998; 98WO-SG000046.
 XX (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 PA Oon CJ, Lim GK, Zhao Y, Chen WN;
 XX WPI; 2000-106104/09.
 DR N-PSDB; AAZ37088.
 DR
 XX New isolated hepatitis B virus strain, useful for, e.g. treatment of
 PT hepatitis infection -
 PT
 XX Disclosure; Page 42; 68pp; English.
 XX
 CC The present sequence is encoded by the genome of an isolated strain of
 CC Hepatitis B virus designated human Hepatitis B virus (HBV) surface
 CC antigen-S'-133 Oon strain (Met to Thr). The viral genome is deposited
 CC as ECCC accession numbers P97121501, P97121502 and P97121503. The
 CC nucleotide sequence was isolated from hepatocellular carcinoma (HCC).
 CC The nucleotide sequence encodes four overlapping proteins, which are

a DNA polymerase, a large surface antigen, a core protein, and a transactivating X protein. The large surface antigen differs from the wild type sequence in that it contains a Thr at position 133 of the wild type sequence instead of a Met. The proteins are used to produce antibodies. The proteins, polynucleotide and antibodies can be used for detecting the novel HBV strain. The HBV polypeptides can also be used in hepatitis vaccines. The HBV novel strain polypeptides can be used to identify compounds for treating or preventing HBV infection or hepatocellular carcinoma.

Sequence 154 AA;

Query Match 94.5%; Score 52; DB 21; Length 154;
Best Local Similarity 88.9%; Pred. No. 0.75;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 CLFKDWEEL 9
:|||||
115 CVFKDWEEL 123

SULT 14
J09615

ABJ09615 standard; Peptide; 9 AA.

ABJ09615;

14-NOV-2002 (first entry)

Hepatitis B virus analogue #227.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 200WO-US24802.

08-SEP-2000; 200WO-US24802.

(EPIM-) EPIMUNE INC.
(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;
Cellis E, Kubo RT, Grey HM, Cheenut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

Disclosure; Page 193; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 9 AA;

Query Match 83.6%; Score 46; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 LFKDWEEL 9
|||||
2 LFKDWEEL 9

RESULT 15

AAP50459

ID AAP50459 standard; Protein; 16 AA.

XX

AC AAP50459;

XX

DT 25-MAR-2003 (updated)

XX

DT 27-SEP-1991 (first entry)

XX

DE Sequence of an antigenic determinant of HBxAg, the antigen

DE encoded by the X region of the hepatitis B virus genome.

XX

KW Hepatitis B virus; X region; antigen; diagnostic assay.

XX

OS Hepatitis B virus.

XX

PN WO8503950-A.

XX

PD 12-SEP-1985.

XX

PF 06-MAR-1985; 85WO-US00359.

XX

PR 07-SEP-1984; 84US-0648142.

XX

PR 08-MAR-1984; 84US-0587570.

XX

PR 26-MAY-1987; 87US-0054424.

XX

PA (SCRI) SCRIPPS CLINIC & RES FOUND.

XX

PI Moriarty AM, Alexander H, Lerner RA;

XX

DR WPI; 1985-236420/38.

XX

PT Expression vector contg. gene coding for hepatitis B HBxAg -

PT useful in diagnostic systems for detection of HBxAg and its

PT antibody in body samples

XX

PS Claim 10ii; Page 83; 86pp; English.

XX

CC The inventors claim an antigenic synthetic polypeptide containing about 6 to about 40 AA residues corresponding in AA residue sequence to an antigenic determinant of HBxAg (see AAP50458-P50460). The

CC antigenic polypeptides may be used in a diagnostic assay system for

CC determining the presence of HBxAg in a body sample.

CC (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 16 AA;

Query Match 83.6%; Score 46; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFKDWEEL 9

|||||

Db 1 LFKDWEEL 8

Search completed: December 23, 2003, 08:44:03
Job time : 27.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

1 protein - protein search, using sw model

on on: December 23, 2003, 08:39:57 ; Search time 25.8 Seconds
(without alignments)
55.370 Million cell updates/sec

file: US-09-989-621-2

effect score: 45

quence: 1 VLHKRTLGL 9

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1107863 seqs, 158726573 residues

tal number of hits satisfying chosen parameters: 1107863

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase : A Geneseq 19Jun03:*

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9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	45	100.0	9 15	AA059193 Peptide fragment (
2	45	100.0	9 20	AA052980 Hepatitis B virus
3	45	100.0	9 20	AA124460 Hepatitis B virus
4	45	100.0	9 23	ABJ06345 Hepatitis B virus
5	45	100.0	9 23	ABJ06875 Hepatitis B virus
6	45	100.0	9 23	ABJ07613 Hepatitis B virus
7	45	100.0	9 23	ABJ08841 Hepatitis B virus
8	45	100.0	9 23	ABJ09133 Hepatitis B virus
9	45	100.0	10 20	AA052970 Hepatitis B virus

10	45	100.0	10 23	ABJ06135 Hepatitis B virus
11	45	100.0	10 23	ABJ06665 Hepatitis B virus
12	45	100.0	10 23	ABJ07674 Hepatitis B virus
13	45	100.0	11 23	ABJ07128 Hepatitis B virus
14	45	100.0	15 23	ABJ08988 Hepatitis B virus
15	45	100.0	15 23	ABJ09280 Hepatitis B virus
16	45	100.0	134 16	AA071563 Sequence of the an
17	45	100.0	154 6	AA050461 Peptide encoded by
18	45	100.0	154 9	AA082174 Hepatitis B virus
19	45	100.0	154 21	AA058473 Human hepatitis B
20	45	100.0	154 21	AA044351 Peptide fragment (
21	42	93.3	9 15	AA059182 Peptide fragment (
22	42	93.3	10 15	AA061555 Hepatitis B virus
23	41	91.1	8 23	AA070034 Antigenic determin
24	41	91.1	22 9	AA082173 Amino acid seque
25	39	86.7	154 21	AA054047 Staphylococcus epi
26	37	82.2	324 23	ABP40151 Drosophila melanog
27	36	80.0	505 22	AB058791 Hepatitis B virus
28	35	77.8	8 23	ABJ06134 Hepatitis B virus
29	35	77.8	8 23	ABJ06664 Hepatitis B virus
30	35	77.8	8 23	ABJ07426 Hepatitis B virus
31	35	77.8	9 23	ABJ07065 Hepatitis B virus
32	35	77.8	10 23	ABJ06965 Hepatitis B virus
33	35	77.8	10 23	ABJ07687 Drosophila melanog
34	35	77.8	144 22	AB058535 Drosophila melanog
35	35	77.8	165 22	AB058534 S cerevisiae apocp
36	35	77.8	452 22	AA070913 Human ORFX ORF452
37	33	73.3	102 21	AA040688 Herbicidally activ
38	33	73.3	143 23	AB093600 Herbicidally activ
39	33	73.3	215 23	AB093441 Mouse immediate ea
40	33	73.3	630 23	AB10103 Drosophila melanog
41	33	73.3	1869 22	AB058651 Human secreted pep
42	32	71.1	23 21	AA028310 Propionibacterium
43	32	71.1	53 22	AA039919 Human ORFX protein
44	32	71.1	90 23	ABP04610 Arabidopsis thalia
45	32	71.1	263 21	AA020271

ALIGNMENTS

RESULT 1

AA059193
ID AA059193 standard; peptide; 9 AA.
XX AA059193;
AC AA059193;
XX
XX 25-MAR-2003 (updated)
DT 03-MAY-1995 (first entry)
XX
XX Peptide fragment (1.0391) of HBV binds HLA-A2.1.

DE
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.

XX Hepatitis B Virus adw.

XX WO9420127-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

PR 04-JUN-1993; 93US-0073205.

PR 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

PI Grey HM, Kast WM, Sette A, Sidney J;

CX WPI; 1994-302678/37.
 CX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 CX for treatment or prophylaxis of cancer, virus infection or
 CX autoimmune diseases.
 CX Example 5; Page 103; 138pp; English.
 CX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
 CX binding motif. These peptides bind HLA-A2.1 and have a binding affinity
 CX of at least 1% as compared to a reference peptide (AAR71293). AAR59193
 CX has an IC50 of 0.0007 and the sequence occurs at position 1539 in the HBV
 CX "X" protein (as given in the specification). The peptides of the
 CX invention can induce cytotoxic T lymphocytes which can react with target
 CX cells. They can be used for the treatment or prophylaxis of cancer, eg.
 CX prostate cancer or lymphoma, etc.
 CX (Updated on 25-MAR-2003 to correct PN field.)
 CX Sequence 9 AA;
 CX
 CX Query Match 100.0%; Score 45; DB 15; Length 9;
 CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX 1 VLHKRTLGL 9
 CX |||||
 CX 1 VLHKRTLGL 9
 CX
 CX RESULT 2
 CX AAM52980
 CX ID AAM52980 standard; peptide; 9 AA.
 CX AC AAM52980;
 CX 12-MAR-2002 (first entry)
 CX Hepatitis B virus X protein peptide (residues 92-100).
 CX HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I;
 CX major histocompatibility complex; immunomodulator.
 CX Hepatitis B virus.
 CX KR98022440-A.
 CX 06-JUL-1998.
 CX 23-SEP-1996; 96KR-0041612.
 CX 23-SEP-1996; 96KR-0041612.
 CX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 CX Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;
 CX WPI; 1999-300977/25.
 CX Synthetic peptide having immunoregulating activities for hepatitis B
 CX virus -
 CX Example 1; Page 4; 7pp; Korean.
 CX The invention relates to peptides derived from the hepatitis B virus
 CX (HBV) X protein (AAM52970-AAM52973). The peptides are presented on major
 CX histocompatibility complex (MHC) class I molecules and act as cytotoxic
 CX T-lymphocyte (CTL) epitopes. Sequences AAM52974-AAM52984 represent HBV
 CX X protein-derived peptides used in an exemplification of the invention.
 CX Sequence 9 AA;
 CX
 CX Query Match 100.0%; Score 45; DB 20; Length 9;

CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX 1 VLHKRTLGL 9
 CX |||||
 CX 1 VLHKRTLGL 9
 CX
 CX RESULT 3
 CX AAY24460
 CX ID AAY24460 standard; peptide; 9 AA.
 CX AC AAY24460;
 CX 23-SEP-1999 (first entry)
 CX Hepatitis B virus X protein peptide #2.
 CX Hepatitis B virus; HBV; X protein; cytotoxic T lymphocyte; liposome;
 CX CTL; antigen; immunity; liver cancer.
 CX Hepatitis B virus.
 CX Synthetic.
 CX W09936434-A1.
 CX 22-JUL-1999.
 CX 19-JAN-1998; 98WO-KR00010.
 CX 19-JAN-1998; 98WO-KR00010.
 CX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
 CX Chang J, Cheong H, Cho S, Choi M, Hwang Y, Kim T;
 CX Lee K;
 CX WPI; 1999-444387/37.
 CX Hepatitis B virus protein X-derived peptide antigens used to
 CX stimulate cytotoxic T lymphocytes, useful for treatment of
 CX HBV-associated diseases, especially liver cancer
 CX Claim 2; Page 24; 33pp; English.
 CX The present invention describes peptide antigens AAY24459 to AAY24463
 CX derived from the X protein of hepatitis B virus (HBV) which are
 CX recognized by cytotoxic T lymphocytes (CTL). The peptide antigens
 CX derived from HBV X protein are useful for inducing CTLs against the
 CX virus or inducing immunological tolerance to the virus. pH-sensitive
 CX liposomes containing the peptide antigens are used to induce cellular
 CX immunity so that CTLs specific to the virus can be produced. This is
 CX useful for prevention and treatment of HBV-associated diseases, permit
 CX especially HBV-associated liver cancer. pH-sensitive liposomes permit
 CX the selective transportation of anti-cancer drugs.
 CX Sequence 9 AA;
 CX
 CX Query Match 100.0%; Score 45; DB 20; Length 9;
 CX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CX
 CX 1 VLHKRTLGL 9
 CX |||||
 CX 1 VLHKRTLGL 9
 CX
 CX RESULT 4
 CX ABJ06345
 CX ID ABJ06345 standard; Peptide; 9 AA.
 CX XX
 CX AC ABJ06345;
 CX XX

14-NOV-2002 (first entry)

Hepatitis B virus epitope #563.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD; Celis E, Kubo RT, Grey HM, Chesnut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

Disclosure; Page 122; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 9 AA;

Query Match 100.0%; Score 45; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. NO. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9

|||||

1 VLHKRTLGL 9

SULT 5

J06875

ABJ06875 standard; Peptide; 9 AA.

ABJ06875;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #1093.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMUNE INC.

(SETT/) SETTE A.

XX

PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;

XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV)

PT infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -

XX Disclosure; Page 131; 228pp; English.

XX The present invention relates to a composition comprising at least one

CC hepatitis B virus epitope. This can be used in the production of a

CC vaccine for use in preventing or treating hepatitis B virus infection.

CC The present sequence is a peptide described in the exemplification of the

CC invention.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 45; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. NO. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLHKRTLGL 9

|||||

1 VLHKRTLGL 9

Db 1 VLHKRTLGL 9

14-NOV-2002 (first entry)

XX Hepatitis B virus epitope #1831.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

KW virucide; hepatotropic; antiinflammatory.

XX Hepatitis B virus.

XX WO200219986-A1.

XX 14-MAR-2002.

XX 08-SEP-2000; 2000WO-US24802.

XX 08-SEP-2000; 2000WO-US24802.

XX (EPIM-) EPIMUNE INC.

XX (SETT/) SETTE A.

XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;

XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV)

PT infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -

XX Disclosure; Page 147; 228pp; English.

XX The present invention relates to a composition comprising at least one

CC hepatitis B virus epitope. This can be used in the production of a

CC vaccine for use in preventing or treating hepatitis B virus infection.

CC The present sequence is a peptide described in the exemplification of the

CC invention.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 45; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. NO. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLHKRTLGL 9

|||||

1 VLHKRTLGL 9

Db 1 VLHKRTLGL 9

14-NOV-2002 (first entry)

XX Hepatitis B virus epitope #1831.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

KW virucide; hepatotropic; antiinflammatory.

XX Hepatitis B virus.

XX WO200219986-A1.

XX 14-MAR-2002.

XX 08-SEP-2000; 2000WO-US24802.

XX 08-SEP-2000; 2000WO-US24802.

XX (EPIM-) EPIMUNE INC.

XX (SETT/) SETTE A.

XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;

XX Celis E, Kubo RT, Grey HM, Chesnut RW;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV)

PT infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -

XX Disclosure; Page 147; 228pp; English.

XX The present invention relates to a composition comprising at least one

CC hepatitis B virus epitope. This can be used in the production of a

CC vaccine for use in preventing or treating hepatitis B virus infection.

CC The present sequence is a peptide described in the exemplification of the

CC invention.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 45; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. NO. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLHKRTLGL 9

|||||

1 VLHKRTLGL 9

Db 1 VLHKRTLGL 9

Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 VLHKRTLGL 9
 |||||
 DB 1 VLHKRTLGL 9

RESULT 7
 ABJ0841
 ID ABJ0841 standard; Peptide; 9 AA.
 AC ABJ0841;
 DT 14-NOV-2002 (first entry)
 DE Hepatitis B virus epitope #3059.
 EW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 EX virucide; hepatotropic; antiinflammatory.
 FS Hepatitis B virus.
 GN WO200219986-A1.
 HP 14-MAR-2002.
 IP 08-SEP-2000; 2000WO-US24802.
 IR 08-SEP-2000; 2000WO-US24802.
 IS (EPIM-) EPIMMUNE INC.
 IT (SETT/) SETTE A.
 JI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 JJ Cellis E, Kubo RT, Grey HM, Chesnut RW;
 KR WPI; 2002-643192/69.
 LV Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -
 Disclosure; Page 178; 228pp; English.
 The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;
 Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VLHKRTLGL 9
 |||||
 b 1 VLHKRTLGL 9

RESULT 8
 BU09133
 ID ABJ09133 standard; Peptide; 9 AA.
 AC ABJ09133;
 DT 14-NOV-2002 (first entry)
 DE Hepatitis B virus epitope #3351.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 OS Hepatitis B virus.
 XX WO200219986-A1.
 XX 14-MAR-2002.
 XX 08-SEP-2000; 2000WO-US24802.
 XX 08-SEP-2000; 2000WO-US24802.
 XX (EPIM-) EPIMMUNE INC.
 XX (SETT/) SETTE A.
 XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Cellis E, Kubo RT, Grey HM, Chesnut RW;
 XX WPI; 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 infection, and/or for stimulating an immune response to HBV, comprises
 a HBV peptide epitope -
 Disclosure; Page 181; 228pp; English.
 The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention.

Sequence 9 AA;
 Query Match 100.0%; Score 45; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLHKRTLGL 9
 |||||
 DB 1 VLHKRTLGL 9

RESULT 9
 AAMS2970
 ID AAMS2970 standard; peptide; 10 AA.
 AC AAMS2970;
 DT 12-MAR-2002 (first entry)
 DE Hepatitis B virus X protein CTL epitope (residues 91-100), SEQ ID NO:1.
 XX HBV; X protein; cytotoxic T-lymphocyte; CTL; MHC class I; epitope;
 KW major histocompatibility complex; immunomodulator.
 XX Hepatitis B virus.
 XX KR98022440-A.
 XX 06-JUL-1998.
 XX 23-SEP-1996; 96KR-0041612.
 XX 23-SEP-1996; 96KR-0041612.
 XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 XX Park SH, Chung MG, Lee HG, Yoon HS, Min SS, Lee TG, Lim JS;
 WPI; 1999-300977/25.

Synthetic peptide having immunoregulating activities for hepatitis B virus

Claim 3; Page 4; 7pp; Korean.

The invention relates to peptides derived from the hepatitis B virus (HBV) X protein (AAM52970-AAM52973). The peptides are presented on major histocompatibility complex (MHC) class I molecules and act as cytotoxic T-lymphocyte (CTL) epitopes. The present sequence represents a specifically claimed HBV X protein CTL epitope of the invention.

Sequence 10 AA;

Query Match 100.0%; Score 45; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9
|||||||
2 VLHKRTLGL 10

ULT 10
06135

ABJ06135 standard; Peptide; 10 AA.

ABJ06135;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #353.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMMUNE INC.

(SETT/) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD; Celis E, Kubo RT, Grey HM, Chesnut RW;

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope

Disclosure; Page 117; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 10 AA;

Query Match 100.0%; Score 45; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9

Db 2 VLHKRTLGL 10
|||||||

RESULT 11

ABJ06665
ID ABJ06665 standard; Peptide; 10 AA.

XX ABJ06665;

XX 14-NOV-2002 (first entry)

XX Hepatitis B virus epitope #883.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

XX Hepatitis B virus.

XX WO200219986-A1.

XX 14-MAR-2002.

XX 08-SEP-2000; 2000WO-US24802.

XX 08-SEP-2000; 2000WO-US24802.

XX (EPIM-) EPIMMUNE INC.

XX (SETT/) SETTE A.

XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD; Celis E, Kubo RT, Grey HM, Chesnut RW;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope

XX Disclosure; Page 128; 228pp; English.

XX The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 45; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHKRTLGL 9

Db 2 VLHKRTLGL 10
|||||||

RESULT 12

ABJ07674
ID ABJ07674 standard; Peptide; 10 AA.

XX ABJ07674;

XX 14-NOV-2002 (first entry)

XX Hepatitis B virus epitope #1892.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

XX Hepatitis B virus.

LT 15
9280
ABJ09280 standard; Peptide; 15 AA.

ABJ09280;

14-NOV-2002 (first entry)

Hepatitis B virus epitope #3498.

Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis; virucide; hepatotropic; antiinflammatory.

Hepatitis B virus.

WO200219986-A1.

14-MAR-2002.

08-SEP-2000; 2000WO-US24802.

08-SEP-2000; 2000WO-US24802.

(EPIM-) EPIMMUNE INC.
(SETT) SETTE A.

Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
Celis E, Kubo RT, Grey HM, Chesnut RW,

WPI; 2002-643192/69.

Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a HBV peptide epitope -

Disclosure; Page 182; 228pp; English.

The present invention relates to a composition comprising at least one hepatitis B virus epitope. This can be used in the production of a vaccine for use in preventing or treating hepatitis B virus infection. The present sequence is a peptide described in the exemplification of the invention.

Sequence 15 AA;

Very Match 100.0%; Score 45; DB 23; Length 15;
Fast Local Similarity 100.0%; Pred. No. 0.0079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VLHKRTLGL 9
|||||||
4 VLHKRTLGL 12

Job completed: December 23, 2003, 08:44:00
Time : 26.8 secs